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(54) Title: POLYPEPTIDES HAVING CELLOBIOHYDROLASE I ACTIVITY AND POLYNUCLEOTIDES ENCODING SAME

(57) Abstract: Abstract The present invention relates to polypeptides having cellobiohydrolase I activity and polynucleotides having a nucleotide sequence which encodes for the polypeptides. The invention also relates to nucleic acid constructs, vectors, and host cells comprising the nucleic acid constructs as well as methods for producing and using the polypeptides.



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**POLYPEPTIDES HAVING CELLOBIOHYDROLASE I ACTIVITY
AND POLYNUCLEOTIDES ENCODING SAME**

Field of the Invention

5 The present invention relates to polypeptides having cellobiohydrolase I (also referred to as CBH I or CBH 1) activity and polynucleotides having a nucleotide sequence which encodes for the polypeptides. The invention also relates to nucleic acid constructs, vectors, and host cells comprising the nucleic acid constructs as well as methods for producing and using the polypeptides.

Background of the Invention

10 Cellulose is an important industrial raw material and a source of renewable energy. The physical structure and morphology of native cellulose are complex and the fine details of its structure have been difficult to determine experimentally. However, the chemical composition of cellulose is simple, consisting of D-glucose residues linked by beta-1,4-glycosidic bonds to form linear polymers with chains length of over 10.000 glycosidic residues.

15 In order to be efficient, the digestion of cellulose requires several types of enzymes acting cooperatively. At least three categories of enzymes are necessary to convert cellulose into glucose: endo (1,4)-beta-D-glucanases (EC 3.2.1.4) that cut the cellulose chains at random; cellobiohydrolases (EC 3.2.1.91) which cleave cellobiosyl units from the cellulose chain ends and beta-glucosidases (EC 3.2.1.21) that convert cellobiose and soluble cellodextrins into glucose. Among these three categories of enzymes involved in the biodegradation of cellulose, cellobiohydrolases are the key enzymes for the degradation of native crystalline cellulose.

20 Exo-cellobiohydrolases (Cellobiohydrolase I, or CBH I) refer to the cellobiohydrolases which degrade cellulose by hydrolyzing the cellobiose from the non-reducing end of the cellulose polymer chains.

25 It is an object of the present invention to provide improved polypeptides having cellobiohydrolase I activity and polynucleotides encoding the polypeptides. The improved polypeptides may have improved specific activity and/or improved stability - in particular improved thermostability. The polypeptides may also have an improved ability to resist inhibition by cellobiose.

Summary of the Invention

30 In a first aspect the present invention relates to a polypeptide having cellobiohydrolase I activity, selected from the group consisting of:

- (a) a polypeptide comprising an amino acid sequence selected from the group consisting of:
- an amino acid sequence which has at least 80% identity with amino acids 1 to 526 of SEQ ID NO:2,
- an amino acid sequence which has at least 80% identity with amino acids 1 to 529 of SEQ ID NO:4,
- an amino acid sequence which has at least 80% identity with amino acids 1 to 451 of SEQ ID NO:6,
- an amino acid sequence which has at least 80% identity with amino acids 1 to 457 of SEQ ID NO:8,
- an amino acid sequence which has at least 80% identity with amino acids 1 to 538 of SEQ ID NO:10,
- an amino acid sequence which has at least 70% identity with amino acids 1 to 415 of SEQ ID NO:12,
- an amino acid sequence which has at least 70% identity with amino acids 1 to 447 of SEQ ID NO:14,
- an amino acid sequence which has at least 80% identity with amino acids 1 to 452 of SEQ ID NO:16,
- an amino acid sequence which has at least 80% identity with amino acids 1 to 454 of SEQ ID NO:38,
- an amino acid sequence which has at least 80% identity with amino acids 1 to 458 of SEQ ID NO:40,
- an amino acid sequence which has at least 80% identity with amino acids 1 to 450 of SEQ ID NO:42,
- an amino acid sequence which has at least 80% identity with amino acids 1 to 446 of SEQ ID NO:44,
- an amino acid sequence which has at least 80% identity with amino acids 1 to 527 of SEQ ID NO:46,
- an amino acid sequence which has at least 80% identity with amino acids 1 to 455 of SEQ ID NO:48,
- an amino acid sequence which has at least 80% identity with amino acids 1 to 464 of SEQ ID NO:50,
- an amino acid sequence which has at least 80% identity with amino acids 1 to 460 of SEQ ID NO:52,
- an amino acid sequence which has at least 80% identity with amino acids 1 to 450 of SEQ ID NO:54,
- an amino acid sequence which has at least 80% identity with amino acids 1 to 532 of SEQ ID NO:56,

an amino acid sequence which has at least 80% identity with amino acids 1 to 460 of SEQ ID NO:58,

an amino acid sequence which has at least 80% identity with amino acids 1 to 525 of SEQ ID NO:60, and

5 an amino acid sequence which has at least 80% identity with amino acids 1 to 456 of SEQ ID NO:66;

(b) a polypeptide comprising an amino acid sequence selected from the group consisting of:
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
10 the cellobiohydrolase I encoding part of the nucleotide sequence present in *Acremonium thermophilum*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Chaetomium thermophilum*,

15 an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Scytalidium* sp.,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Scytalidium*
20 *thermophilum*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Thermoascus aurantiacus*,

25 an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Thielavia australiensis*,

an amino acid sequence which has at least 70% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Verticillium tenerum*,

30 an amino acid sequence which has at least 70% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Neotermes castaneus*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in
35 *Melanocarpus albomyces*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in

Acremonium sp.,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Chaetomidium pingtungium*,

5 an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Sporotrichum pruinosum*,

10 an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Diplodia gossypina*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Trichophaea saccata*,

15 an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Myceliophthora thermophila*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Exidia glandulosa*,

20 an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Xylaria hypoxylon*,

25 an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Poitrasia circinans*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Coprinus cinereus*,

30 an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Pseudoplectania nigrella*,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Trichothecium roseum* IFO 5372,

35 an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Humicola nigrescens* CBS 819.73,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Cladorrhinum foecundissimum* CBS 427.97,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Diplodia gossypina* CBS 247.96,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Myceliophthora thermophila* CBS 117.65,

5 an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Rhizomucor pusillus* CBS 109471,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Meripilus giganteus* CBS 521.95,

10 an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Exidia glandulosa* CBS 2377.96,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Xylaria hypoxylon* CBS 284.96,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Trichophaea saccata* CBS 804.70,

15 an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Chaetomium* sp.,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Myceliophthora hinnulea*,

20 an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Thielavia cf. microspora*,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Aspergillus* sp.,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Scopulariopsis* sp.,

25 an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Fusarium* sp.,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Verticillium* sp., and

30 an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Phytophthora infestans*;

(c) a polypeptide comprising an amino acid sequence selected from the group consisting of:
an amino acid sequence which has at least 80% identity with the polypeptide encoded by nucleotides 1 to 1578 of SEQ ID NO:1,

35 an amino acid sequence which has at least 80% identity with the polypeptide encoded by nucleotides 1 to 1587 of SEQ ID NO:3,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by

nucleotides 1 to 1353 of SEQ ID NO:5,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1371 of SEQ ID NO:7,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
5 nucleotides 1 to 1614 of SEQ ID NO:9,
an amino acid sequence which has at least 70% identity with the polypeptide encoded by
nucleotides 1 to 1245 of SEQ ID NO:11,
an amino acid sequence which has at least 70% identity with the polypeptide encoded by
nucleotides 1 to 1341 of SEQ ID NO:13,
10 an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1356 of SEQ ID NO:15,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1365 of SEQ ID NO:37,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
15 nucleotides 1 to 1377 of SEQ ID NO:39,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1353 of SEQ ID NO:41,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1341 of SEQ ID NO:43,
20 an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1584 of SEQ ID NO:45,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1368 of SEQ ID NO:47,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
25 nucleotides 1 to 1395 of SEQ ID NO:49,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1383 of SEQ ID NO:51,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1353 of SEQ ID NO:53,
30 an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1599 of SEQ ID NO:55,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1383 of SEQ ID NO:57,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
35 nucleotides 1 to 1578 of SEQ ID NO:59, and
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1371 of SEQ ID NO:65;

(d) a polypeptide which is encoded by a nucleotide sequence which hybridizes under high stringency conditions with a polynucleotide probe selected from the group consisting of:

(i) the complementary strand of the nucleotides selected from the group consisting of:

5 nucleotides 1 to 1578 of SEQ ID NO:1,
 nucleotides 1 to 1587 of SEQ ID NO:3,
 nucleotides 1 to 1353 of SEQ ID NO:5,
 nucleotides 1 to 1371 of SEQ ID NO:7,
 nucleotides 1 to 1614 of SEQ ID NO:9,
 10 nucleotides 1 to 1245 of SEQ ID NO:11,
 nucleotides 1 to 1341 of SEQ ID NO:13,
 nucleotides 1 to 1356 of SEQ ID NO:15,
 nucleotides 1 to 1365 of SEQ ID NO:37,
 nucleotides 1 to 1377 of SEQ ID NO:39,
 15 nucleotides 1 to 1353 of SEQ ID NO:41,
 nucleotides 1 to 1341 of SEQ ID NO:43,
 nucleotides 1 to 1584 of SEQ ID NO:45,
 nucleotides 1 to 1368 of SEQ ID NO:47,
 nucleotides 1 to 1395 of SEQ ID NO:49,
 20 nucleotides 1 to 1383 of SEQ ID NO:51,
 nucleotides 1 to 1353 of SEQ ID NO:53,
 nucleotides 1 to 1599 of SEQ ID NO:55,
 nucleotides 1 to 1383 of SEQ ID NO:57,
 nucleotides 1 to 1578 of SEQ ID NO:59, and
 25 nucleotides 1 to 1371 of SEQ ID NO:65;

(ii) the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 1 to 500 of SEQ ID NO:1,
 nucleotides 1 to 500 of SEQ ID NO:3,
 nucleotides 1 to 500 of SEQ ID NO:5,
 30 nucleotides 1 to 500 of SEQ ID NO:7,
 nucleotides 1 to 500 of SEQ ID NO:9,
 nucleotides 1 to 500 of SEQ ID NO:11,
 nucleotides 1 to 500 of SEQ ID NO:13,
 nucleotides 1 to 500 of SEQ ID NO:15,
 35 nucleotides 1 to 500 of SEQ ID NO:37,
 nucleotides 1 to 500 of SEQ ID NO:39,
 nucleotides 1 to 500 of SEQ ID NO:41,

- 5 nucleotides 1 to 500 of SEQ ID NO:43,
 nucleotides 1 to 500 of SEQ ID NO:45,
 nucleotides 1 to 500 of SEQ ID NO:47,
 nucleotides 1 to 500 of SEQ ID NO:49,
 nucleotides 1 to 500 of SEQ ID NO:51,
 nucleotides 1 to 500 of SEQ ID NO:53,
 nucleotides 1 to 500 of SEQ ID NO:55,
 nucleotides 1 to 500 of SEQ ID NO:57,
 nucleotides 1 to 500 of SEQ ID NO:59,
 10 nucleotides 1 to 500 of SEQ ID NO:65,
 nucleotides 1 to 221 of SEQ ID NO:17,
 nucleotides 1 to 239 of SEQ ID NO:18,
 nucleotides 1 to 199 of SEQ ID NO:19,
 nucleotides 1 to 191 of SEQ ID NO:20,
 15 nucleotides 1 to 232 of SEQ ID NO:21,
 nucleotides 1 to 467 of SEQ ID NO:22,
 nucleotides 1 to 534 of SEQ ID NO:23,
 nucleotides 1 to 563 of SEQ ID NO:24,
 nucleotides 1 to 218 of SEQ ID NO:25,
 20 nucleotides 1 to 492 of SEQ ID NO:26,
 nucleotides 1 to 481 of SEQ ID NO:27,
 nucleotides 1 to 463 of SEQ ID NO:28,
 nucleotides 1 to 513 of SEQ ID NO:29,
 nucleotides 1 to 579 of SEQ ID NO:30,
 25 nucleotides 1 to 514 of SEQ ID NO:31,
 nucleotides 1 to 477 of SEQ ID NO:32,
 nucleotides 1 to 500 of SEQ ID NO:33,
 nucleotides 1 to 470 of SEQ ID NO:34,
 nucleotides 1 to 491 of SEQ ID NO:35,
 30 nucleotides 1 to 221 of SEQ ID NO:36,
 nucleotides 1 to 519 of SEQ ID NO:61,
 nucleotides 1 to 497 of SEQ ID NO:62,
 nucleotides 1 to 498 of SEQ ID NO:63,
 nucleotides 1 to 525 of SEQ ID NO:64, and
 35 nucleotides 1 to 951 of SEQ ID NO:67; and
- (iii) the complementary strand of the nucleotides selected from the group consisting of:
 nucleotides 1 to 200 of SEQ ID NO:1,

5 nucleotides 1 to 200 of SEQ ID NO:3,
nucleotides 1 to 200 of SEQ ID NO:5,
nucleotides 1 to 200 of SEQ ID NO:7,
nucleotides 1 to 200 of SEQ ID NO:9,
nucleotides 1 to 200 of SEQ ID NO:11,
nucleotides 1 to 200 of SEQ ID NO:13,
nucleotides 1 to 200 of SEQ ID NO:15,
nucleotides 1 to 200 of SEQ ID NO:37,
nucleotides 1 to 200 of SEQ ID NO:39,
10 nucleotides 1 to 200 of SEQ ID NO:41,
nucleotides 1 to 200 of SEQ ID NO:43,
nucleotides 1 to 200 of SEQ ID NO:45,
nucleotides 1 to 200 of SEQ ID NO:47,
nucleotides 1 to 200 of SEQ ID NO:49,
15 nucleotides 1 to 200 of SEQ ID NO:51,
nucleotides 1 to 200 of SEQ ID NO:53,
nucleotides 1 to 200 of SEQ ID NO:55,
nucleotides 1 to 200 of SEQ ID NO:57,
nucleotides 1 to 200 of SEQ ID NO:59, and
20 nucleotides 1 to 200 of SEQ ID NO:65; and

(e) a fragment of (a), (b) or (c) that has cellobiohydrolase I activity.

25 In a second aspect the present invention relates to a polynucleotide having a nucleotide sequence which encodes for the polypeptide of the invention.

In a third aspect the present invention relates to a nucleic acid construct comprising the nucleotide sequence, which encodes for the polypeptide of the invention, operably linked to one or more control sequences that direct the production of the polypeptide in a suitable host.

30 In a fourth aspect the present invention relates to a recombinant expression vector comprising the nucleic acid construct of the invention.

In a fifth aspect the present invention relates to a recombinant host cell comprising the nucleic acid construct of the invention.

In a sixth aspect the present invention relates to a method for producing a polypeptide of the invention, the method comprising:

- 35 (a) cultivating a strain, which in its wild-type form is capable of producing the polypeptide, to produce the polypeptide; and
(b) recovering the polypeptide.

In a seventh aspect the present invention relates to a method for producing a polypeptide of the invention, the method comprising:

- (a) cultivating a recombinant host cell of the invention under conditions conducive for production of the polypeptide; and
- 5 (b) recovering the polypeptide.

In an eighth aspect the present invention relates to a method for in-situ production of a polypeptide of the invention, the method comprising:

- (a) cultivating a recombinant host cell of the invention under conditions conducive for production of the polypeptide; and
- 10 (b) contacting the polypeptide with a desired substrate without prior recovery of the polypeptide.

Other aspects of the present invention will be apparent from the below description and from the appended claims.

Definitions

Prior to discussing the present invention in further details, the following terms and conventions will first be defined:

Substantially pure polypeptide: In the present context, the term "substantially pure polypeptide" means a polypeptide preparation which contains at the most 10% by weight of other polypeptide material with which it is natively associated (lower percentages of other polypeptide material are preferred, e.g. at the most 8% by weight, at the most 6% by weight, at the most 5% by weight, at the most 4% at the most 3% by weight, at the most 2% by weight, at the most 1% by weight, and at the most ½% by weight). Thus, it is preferred that the substantially pure polypeptide is at least 92% pure, i.e. that the polypeptide constitutes at least 92% by weight of the total polypeptide material present in the preparation, and higher percentages are preferred such as at least 94% pure, at least 95% pure, at least 96% pure, at least 96% pure, at least 97% pure, at least 98% pure, at least 99%, and at the most 99.5% pure. The polypeptides disclosed herein are preferably in a substantially pure form. In particular, it is preferred that the polypeptides disclosed herein are in "essentially pure form", i.e. that the polypeptide preparation is essentially free of other polypeptide material with which it is natively associated. This can be accomplished, for example, by preparing the polypeptide by means of well-known recombinant methods. Herein, the term "substantially pure polypeptide" is synonymous with the terms "isolated polypeptide" and "polypeptide in isolated form".

Cellobiohydrolase I activity: The term "cellobiohydrolase I activity" is defined herein as a cellulose 1,4-beta-cellobiosidase (also referred to as Exo-glucanase, Exo-cellobiohydrolase or

1,4-beta-cellobiohydrolase) activity, as defined in the enzyme class EC 3.2.1.91, which catalyzes the hydrolysis of 1,4-beta-D-glucosidic linkages in cellulose and cellotetraose, releasing cellobiose from the non-reducing ends of the chains.

For purposes of the present invention, cellobiohydrolase I activity may be determined according to the procedure described in Example 2.

In an embodiment, cellobiohydrolase I activity may be determined according to the procedure described in Deshpande MV et al., *Methods in Enzymology*, pp. 126-130 (1988): "Selective Assay for Exo-1,4-Beta-Glucanases". According to this procedure, one unit of cellobiohydrolase I activity (agluconic bond cleavage activity) is defined as 1.0 μ mole of *p*-nitrophenol produced per minute at 50°C, pH 5.0.

The polypeptides of the present invention should preferably have at least 20% of the cellobiohydrolase I activity of a polypeptide consisting of an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66. In a particular preferred embodiment, the polypeptides should have at least 40%, such as at least 50%, preferably at least 60%, such as at least 70%, more preferably at least 80%, such as at least 90%, most preferably at least 95%, such as about or at least 100% of the cellobiohydrolase I activity of the polypeptide consisting of the amino acid sequence selected from the group consisting of amino acids 1 to 526 of SEQ ID NO:2, amino acids 1 to 529 of SEQ ID NO:4, amino acids 1 to 451 of SEQ ID NO:6, amino acids 1 to 457 of SEQ ID NO:8, amino acids 1 to 538 of SEQ ID NO:10, amino acids 1 to 415 of SEQ ID NO:12, amino acids 1 to 447 of SEQ ID NO:14, amino acids 1 to 452 of SEQ ID NO:16, amino acids 1 to 454 of SEQ ID NO:38, amino acids 1 to 458 of SEQ ID NO:40, amino acids 1 to 450 of SEQ ID NO:42, amino acids 1 to 446 of SEQ ID NO:44, amino acids 1 to 527 of SEQ ID NO:46, amino acids 1 to 455 of SEQ ID NO:48, amino acids 1 to 464 of SEQ ID NO:50, amino acids 1 to 460 of SEQ ID NO:52, amino acids 1 to 450 of SEQ ID NO:54, amino acids 1 to 532 of SEQ ID NO:56, amino acids 1 to 460 of SEQ ID NO:58, amino acids 1 to 525 of SEQ ID NO:60, and amino acids 1 to 456 of SEQ ID NO:66.

Identity: In the present context, the homology between two amino acid sequences or between two nucleotide sequences is described by the parameter "identity".

For purposes of the present invention, the degree of identity between two amino acid sequences is determined by using the program FASTA included in version 2.0x of the FASTA program package (see W. R. Pearson and D. J. Lipman (1988), "Improved Tools for Biological Sequence Analysis", PNAS 85:2444-2448; and W. R. Pearson (1990) "Rapid and Sensitive Sequence Comparison with FASTP and FASTA", *Methods in Enzymology* 183:63-98). The

scoring matrix used was BLOSUM50, gap penalty was -12, and gap extension penalty was -2.

The degree of identity between two nucleotide sequences is determined using the same algorithm and software package as described above. The scoring matrix used was the identity matrix, gap penalty was -16, and gap extension penalty was -4.

5 Fragment: When used herein, a "fragment" of a sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66 is a polypeptide
10 having one or more amino acids deleted from the amino and/or carboxyl terminus of this amino acid sequence. Preferably, a fragment is a polypeptide having the amino acid sequence deleted corresponding to the "cellulose-binding domain" and/or the "linker domain" of *Trichoderma reesei* cellobiohydrolase I as described in SWISS-PROT accession number P00725. More preferably, a fragment comprises the amino acid sequence corresponding to
15 the "catalytic domain" of *Trichoderma reesei* cellobiohydrolase I as described in SWISS-PROT accession number P00725. Most preferably, a fragment contains at least 434 amino acid residues, e.g., the amino acid residues selected from the group consisting of amino acids 1 to 434 of SEQ ID NO:2, amino acids 1 to 434 of SEQ ID NO:4, amino acids 1 to 434 of SEQ ID NO:6, amino acids 1 to 434 of SEQ ID NO:8, amino acids 1 to 434 of SEQ ID NO:10, amino acids 1 to 434 of SEQ ID NO:14, amino acids 1 to 434 of SEQ ID NO:16, amino acids 1 to 434 of SEQ ID NO:38, amino acids 1 to 434 of SEQ ID NO:40, amino acids 1 to 434 of SEQ ID NO:42, amino acids 1 to 434 of SEQ ID NO:44, amino acids 1 to 434 of SEQ ID NO:46, amino acids 1 to 434 of SEQ ID NO:48, amino acids 1 to 434 of SEQ ID NO:50, amino acids 1 to 434 of SEQ ID NO:52, amino acids 1 to 434 of SEQ ID NO:54, amino acids 1 to 434 of SEQ ID NO:56, amino acids 1 to 434 of SEQ ID NO:58, amino acids 1 to 434 of SEQ ID NO:60, and amino acids 1 to 434 of SEQ ID NO:66. In particular, a fragment contains at least 215 amino acid residues, e.g., the amino acid residues selected from the group consisting of amino acids 200 to 434 of SEQ ID NO:2, amino acids 200 to 434 of SEQ ID NO:4, amino acids 200 to 434 of SEQ ID NO:6, amino acids 200 to 434 of SEQ ID NO:8, amino acids 200 to 434 of SEQ ID NO:10, amino acids 200 to 415 of SEQ ID NO:12, amino acids 200 to 434 of SEQ ID NO:14, amino acids 200 to 434 of SEQ ID NO:16, amino acids 200 to 434 of SEQ ID NO:38, amino acids 200 to 434 of SEQ ID NO:40, amino acids 200 to 434 of SEQ ID NO:42, amino acids 200 to 434 of SEQ ID NO:44, amino acids 200 to 434 of SEQ ID NO:46, amino acids 200 to 434 of SEQ ID NO:48, amino acids 200 to 434 of SEQ ID NO:50, amino acids 200 to 434 of SEQ ID NO:52, amino acids 200 to 434 of SEQ ID NO:54, amino acids 200 to 434 of SEQ ID NO:56, amino acids 200 to 434 of SEQ ID NO:58, amino acids 200 to 434 of SEQ ID NO:60, and amino acids 200 to 434 of SEQ ID NO:66.

Allelic variant: In the present context, the term "allelic variant" denotes any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally through mutation, and may result in polymorphism within populations. Gene mutations can be silent (no change in the encoded polypeptide) or may encode polypeptides having altered amino acid sequences. An allelic variant of a polypeptide is a polypeptide encoded by an allelic variant of a gene.

Substantially pure polynucleotide: The term "substantially pure polynucleotide" as used herein refers to a polynucleotide preparation, wherein the polynucleotide has been removed from its natural genetic milieu, and is thus free of other extraneous or unwanted coding sequences and is in a form suitable for use within genetically engineered protein production systems. Thus, a substantially pure polynucleotide contains at the most 10% by weight of other polynucleotide material with which it is natively associated (lower percentages of other polynucleotide material are preferred, e.g. at the most 8% by weight, at the most 6% by weight, at the most 5% by weight, at the most 4% at the most 3% by weight, at the most 2% by weight, at the most 1% by weight, and at the most ½% by weight). A substantially pure polynucleotide may, however, include naturally occurring 5' and 3' untranslated regions, such as promoters and terminators. It is preferred that the substantially pure polynucleotide is at least 92% pure, i.e. that the polynucleotide constitutes at least 92% by weight of the total polynucleotide material present in the preparation, and higher percentages are preferred such as at least 94% pure, at least 95% pure, at least 96% pure, at least 96% pure, at least 97% pure, at least 98% pure, at least 99%, and at the most 99.5% pure. The polynucleotides disclosed herein are preferably in a substantially pure form. In particular, it is preferred that the polynucleotides disclosed herein are in "essentially pure form", i.e. that the polynucleotide preparation is essentially free of other polynucleotide material with which it is natively associated. Herein, the term "substantially pure polynucleotide" is synonymous with the terms "isolated polynucleotide" and "polynucleotide in isolated form".

Modification(s): In the context of the present invention the term "modification(s)" is intended to mean any chemical modification of a polypeptide consisting of an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66, as well as genetic manipulation of the DNA encoding that polypeptide. The modification(s) can be replacement(s) of the amino acid side chain(s), substitution(s), deletion(s) and/or insertions(s) in or at the amino acid(s) of interest.

Artificial variant: When used herein, the term "artificial variant" means a polypeptide having cellobiohydrolase I activity, which has been produced by an organism which is

expressing a modified gene as compared to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, or SEQ ID NO:65. The modified gene, from which said variant is produced when expressed in a suitable host, is obtained through human intervention by modification of a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, and SEQ ID NO:65.

cDNA: The term "cDNA" when used in the present context, is intended to cover a DNA molecule which can be prepared by reverse transcription from a mature, spliced, mRNA molecule derived from a eukaryotic cell. cDNA lacks the intron sequences that are usually present in the corresponding genomic DNA. The initial, primary RNA transcript is a precursor to mRNA and it goes through a series of processing events before appearing as mature spliced mRNA. These events include the removal of intron sequences by a process called splicing. When cDNA is derived from mRNA it therefore lacks intron sequences.

Nucleic acid construct: When used herein, the term "nucleic acid construct" means a nucleic acid molecule, either single- or double-stranded, which is isolated from a naturally occurring gene or which has been modified to contain segments of nucleic acids in a manner that would not otherwise exist in nature. The term nucleic acid construct is synonymous with the term "expression cassette" when the nucleic acid construct contains the control sequences required for expression of a coding sequence of the present invention.

Control sequence: The term "control sequences" is defined herein to include all components, which are necessary or advantageous for the expression of a polypeptide of the present invention. Each control sequence may be native or foreign to the nucleotide sequence encoding the polypeptide. Such control sequences include, but are not limited to, a leader, polyadenylation sequence, propeptide sequence, promoter, signal peptide sequence, and transcription terminator. At a minimum, the control sequences include a promoter, and transcriptional and translational stop signals. The control sequences may be provided with linkers for the purpose of introducing specific restriction sites facilitating ligation of the control sequences with the coding region of the nucleotide sequence encoding a polypeptide.

Operably linked: The term "operably linked" is defined herein as a configuration in which a control sequence is appropriately placed at a position relative to the coding sequence of the DNA sequence such that the control sequence directs the expression of a polypeptide.

Coding sequence: When used herein the term "coding sequence" is intended to cover a

nucleotide sequence, which directly specifies the amino acid sequence of its protein product. The boundaries of the coding sequence are generally determined by an open reading frame, which usually begins with the ATG start codon. The coding sequence typically include DNA, cDNA, and recombinant nucleotide sequences.

5 Expression: In the present context, the term "expression" includes any step involved in the production of the polypeptide including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

10 Expression vector: In the present context, the term "expression vector" covers a DNA molecule, linear or circular, that comprises a segment encoding a polypeptide of the invention, and which is operably linked to additional segments that provide for its transcription.

Host cell: The term "host cell", as used herein, includes any cell type which is susceptible to transformation with a nucleic acid construct.

15 The terms "polynucleotide probe", "hybridization" as well as the various stringency conditions are defined in the section entitled "Polypeptides Having Cellobiohydrolase I Activity".

Thermostability: The term "thermostability", as used herein, is measured as described in Example 2.

Detailed Description of the Invention

20

Polypeptides Having Cellobiohydrolase I Activity

In a first embodiment, the present invention relates to polypeptides having cellobiohydrolase I activity and where the polypeptides comprises, preferably consists of, an amino acid sequence which has a degree of identity to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66, (*i.e.*, the mature polypeptide) of at least 65%, preferably at least 70%, e.g. at least 75%, more preferably at least 80%, such as at least 85%, even more preferably at least 90%, most preferably at least 95%, e.g. at least 96%, such as at least 97%, and even most preferably at least 98%, such as at least 99% (hereinafter "homologous polypeptides"). In an interesting embodiment, the amino acid sequence differs by at the most ten amino acids (e.g. by ten amino acids), in particular by at the most five amino acids (e.g. by five amino acids), such as by at the most four amino acids (e.g. by four amino acids), e.g. by at the most three amino acids (e.g. by three amino acids) from an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ

ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66. In a particular interesting embodiment, the amino acid sequence differs by at the most two amino acids (e.g. by two amino acids), such as by one amino acid from an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66.

Preferably, the polypeptides of the present invention comprise an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66; an allelic variant thereof; or a fragment thereof that has cellobiohydrolase I activity. In another preferred embodiment, the polypeptide of the present invention consists of an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66.

The polypeptide of the invention may be a wild-type cellobiohydrolase I identified and isolated from a natural source. Such wild-type polypeptides may be specifically screened for by standard techniques known in the art, such as molecular screening as described in Example 1. Furthermore, the polypeptide of the invention may be prepared by the DNA shuffling technique, such as described in J.E. Ness et al. *Nature Biotechnology* **17**, 893-896 (1999). Moreover, the polypeptide of the invention may be an artificial variant which comprises, preferably consists of, an amino acid sequence that has at least one substitution, deletion and/or insertion of an amino acid as compared to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66. Such artificial variants may be constructed by standard techniques known in the art, such as by site-directed/random mutagenesis of the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40,

SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66.

In one embodiment of the invention, amino acid changes (in the artificial variant as well as in wild-type polypeptides) are of a minor nature, that is conservative amino acid substitutions that do not significantly affect the folding and/or activity of the protein; small deletions, typically of one to about 30 amino acids; small amino- or carboxyl-terminal extensions, such as an amino-terminal methionine residue; a small linker peptide of up to about 20-25 residues; or a small extension that facilitates purification by changing net charge or another function, such as a poly-histidine tract, an antigenic epitope or a binding domain.

Examples of conservative substitutions are within the group of basic amino acids (arginine, lysine and histidine), acidic amino acids (glutamic acid and aspartic acid), polar amino acids (glutamine and asparagine), hydrophobic amino acids (leucine, isoleucine, valine and methionine), aromatic amino acids (phenylalanine, tryptophan and tyrosine), and small amino acids (glycine, alanine, serine and threonine). Amino acid substitutions which do not generally alter the specific activity are known in the art and are described, for example, by H. Neurath and R.L. Hill, 1979, *In, The Proteins*, Academic Press, New York. The most commonly occurring exchanges are Ala/Ser, Val/Ile, Asp/Glu, Thr/Ser, Ala/Gly, Ala/Thr, Ser/Asn, Ala/Val, Ser/Gly, Tyr/Phe, Ala/Pro, Lys/Arg, Asp/Asn, Leu/Ile, Leu/Val, Ala/Glu, and Asp/Gly as well as these in reverse.

In an interesting embodiment of the invention, the amino acid changes are of such a nature that the physico-chemical properties of the polypeptides are altered. For example, amino acid changes may be performed, which improve the thermal stability of the polypeptide, which alter the substrate specificity, which changes the pH optimum, and the like.

Preferably, the number of such substitutions, deletions and/or insertions as compared to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66 is at the most 10, such as at the most 9, e.g. at the most 8, more preferably at the most 7, e.g. at the most 6, such as at the most 5, most preferably at the most 4, e.g. at the most 3, such as at the most 2, in particular at the most 1.

The present inventors have isolated nucleotide sequences encoding polypeptides having cellobiohydrolase I activity from the microorganisms selected from the group consisting of *Acremonium thermophilum*, *Chaetomium thermophilum*, *Scytalidium* sp., *Scytalidium thermophilum*, *Thermoascus aurantiacus*, *Thielavia australiensis*, *Verticillium tenerum*, *Melanocarpus albomyces*, *Poitrasia circinans*, *Coprinus cinereus*, *Trichothecium roseum*, *Humicola nigrescens*, *Cladorrhinum foecundissimum*, *Diplodia gossypina*, *Myceliophthora*

thermophila, *Rhizomucor pusillus*, *Meripilus giganteus*, *Exidia glandulosa*, *Xylaria hypoxylon*,
Trichophaea saccata, *Acremonium* sp., *Chaetomium* sp., *Chaetomidium pingtungium*,
Myceliophthora thermophila, *Myceliophthora hinnulea*, *Sporotrichum pruinosum*, *Thielavia* cf.
microspora, *Aspergillus* sp., *Scopulariopsis* sp., *Fusarium* sp., *Verticillium* sp.,
5 *Pseudoplectania nigrella*, and *Phytophthora infestans*; and from the gut of the termite larvae
Neotermes castaneus. Thus, in a second embodiment, the present invention relates to
polypeptides comprising an amino acid sequence which has at least 65% identity with the
polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence
present in an organism selected from the group consisting of *Acremonium thermophilum*,
10 *Chaetomium thermophilum*, *Scytalidium* sp., *Scytalidium thermophilum*, *Thermoascus*
aurantiacus, *Thielavia australiensis*, *Verticillium tenerum*, *Neotermes castaneus*,
Melanocarpus albomyces, *Poitrasia circinans*, *Coprinus cinereus*, *Trichothecium roseum* IFO
5372, *Humicola nigrescens* CBS 819.73, *Cladorrhinum foecundissimum* CBS 427.97, *Diplodia*
gossypina CBS 247.96, *Myceliophthora thermophila* CBS 117.65, *Rhizomucor pusillus* CBS
15 109471, *Meripilus giganteus* CBS 521.95, *Exidia glandulosa* CBS 2377.96, *Xylaria hypoxylon*
CBS 284.96, *Trichophaea saccata* CBS 804.70, *Acremonium* sp., *Chaetomium* sp.,
Chaetomidium pingtungium, *Myceliophthora thermophila*, *Myceliophthora hinnulea*,
Sporotrichum pruinosum, *Thielavia* cf. *microspora*, *Aspergillus* sp., *Scopulariopsis* sp.,
Fusarium sp., *Verticillium* sp., *Pseudoplectania nigrella*, and *Phytophthora infestans*. In an
20 interesting embodiment of the invention, the polypeptide comprises an amino acid sequence
which has at least 70%, e.g. at least 75%, preferably at least 80%, such as at least 85%, more
preferably at least 90%, most preferably at least 95%, e.g. at least 96%, such as at least 97%,
and even most preferably at least 98%, such as at least 99% identity with the polypeptide
encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in an
25 organism selected from the group consisting of *Acremonium thermophilum*, *Chaetomium*
thermophilum, *Scytalidium* sp., *Scytalidium thermophilum*, *Thermoascus aurantiacus*,
Thielavia australiensis, *Verticillium tenerum*, *Neotermes castaneus*, *Melanocarpus albomyces*,
Poitrasia circinans, *Coprinus cinereus*, *Trichothecium roseum* IFO 5372, *Humicola nigrescens*
CBS 819.73, *Cladorrhinum foecundissimum* CBS 427.97, *Diplodia gossypina* CBS 247.96,
30 *Myceliophthora thermophila* CBS 117.65, *Rhizomucor pusillus* CBS 109471, *Meripilus*
giganteus CBS 521.95, *Exidia glandulosa* CBS 2377.96, *Xylaria hypoxylon* CBS 284.96,
Trichophaea saccata CBS 804.70, *Acremonium* sp., *Chaetomium* sp., *Chaetomidium*
pingtungium, *Myceliophthora thermophila*, *Myceliophthora hinnulea*, *Sporotrichum pruinosum*,
Thielavia cf. *microspora*, *Aspergillus* sp., *Scopulariopsis* sp., *Fusarium* sp., *Verticillium* sp.,
35 *Pseudoplectania nigrella*, and *Phytophthora infestans* (hereinafter "homologous
polypeptides"). In an interesting embodiment, the amino acid sequence differs by at the most
ten amino acids (e.g. by ten amino acids), in particular by at the most five amino acids (e.g. by

five amino acids), such as by at the most four amino acids (e.g. by four amino acids), e.g. by at the most three amino acids (e.g. by three amino acids) from the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in an organism selected from the group consisting of *Acremonium thermophilum*, *Chaetomium thermophilum*, *Scytalidium* sp., *Scytalidium thermophilum*, *Thermoascus aurantiacus*, *Thielavia australiensis*, *Verticillium tenerum*, *Neotermes castaneus*, *Melanocarpus albomyces*, *Poitrasia circinans*, *Coprinus cinereus*, *Trichothecium roseum* IFO 5372, *Humicola nigrescens* CBS 819.73, *Cladorrhinum foecundissimum* CBS 427.97, *Diplodia gossypina* CBS 247.96, *Myceliophthora thermophila* CBS 117.65, *Rhizomucor pusillus* CBS 109471, *Meripilus giganteus* CBS 521.95, *Exidia glandulosa* CBS 2377.96, *Xylaria hypoxylon* CBS 284.96, *Trichophaea saccata* CBS 804.70, *Acremonium* sp., *Chaetomium* sp., *Chaetomidium pingtungium*, *Myceliophthora thermophila*, *Myceliophthora hinnulea*, *Sporotrichum pruinosum*, *Thielavia cf. microspora*, *Aspergillus* sp., *Scopulariopsis* sp., *Fusarium* sp., *Verticillium* sp., *Pseudoplectania nigrella*, and *Phytophthora infestans*. In a particular interesting embodiment, the amino acid sequence differs by at the most two amino acids (e.g. by two amino acids), such as by one amino acid from the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in an organism selected from the group consisting of *Acremonium thermophilum*, *Chaetomium thermophilum*, *Scytalidium* sp., *Scytalidium thermophilum*, *Thermoascus aurantiacus*, *Thielavia australiensis*, *Verticillium tenerum*, *Neotermes castaneus*, *Melanocarpus albomyces*, *Poitrasia circinans*, *Coprinus cinereus*, *Trichothecium roseum* IFO 5372, *Humicola nigrescens* CBS 819.73, *Cladorrhinum foecundissimum* CBS 427.97, *Diplodia gossypina* CBS 247.96, *Myceliophthora thermophila* CBS 117.65, *Rhizomucor pusillus* CBS 109471, *Meripilus giganteus* CBS 521.95, *Exidia glandulosa* CBS 2377.96, *Xylaria hypoxylon* CBS 284.96, *Trichophaea saccata* CBS 804.70, *Acremonium* sp., *Chaetomium* sp., *Chaetomidium pingtungium*, *Myceliophthora thermophila*, *Myceliophthora hinnulea*, *Sporotrichum pruinosum*, *Thielavia cf. microspora*, *Aspergillus* sp., *Scopulariopsis* sp., *Fusarium* sp., *Verticillium* sp., *Pseudoplectania nigrella*, and *Phytophthora infestans*.

Preferably, the polypeptides of the present invention comprise the amino acid sequence of the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in a deposited microorganism selected from the group consisting of CGMCC No. 0584, CGMCC No. 0581, CGMCC No. 0585, CGMCC No. 0582, CGMCC No. 0583, CBS 109513, DSM 14348, CGMCC No. 0580, DSM 15064, DSM 15065, DSM 15066, DSM 15067, CGMCC No. 0747, CGMCC No. 0748, CGMCC No. 0749, and CGMCC No. 0750. In another preferred embodiment, the polypeptide of the present invention consists of the amino acid sequence of the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in a deposited microorganism selected from the group consisting of CGMCC No. 0584, CGMCC

No. 0581, CGMCC No. 0585, CGMCC No. 0582, CGMCC No. 0583, CBS 109513, DSM 14348, and CGMCC No. 0580, DSM 15064, DSM 15065, DSM 15066, DSM 15067, CGMCC No. 0747, CGMCC No. 0748, CGMCC No. 0749, and CGMCC No. 0750.

5 In a similar way as described above, the polypeptide of the invention may be an artificial variant which comprises, preferably consists of, an amino acid sequence that has at least one substitution, deletion and/or insertion of an amino acid as compared to the amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in a deposited microorganism selected from the group consisting of CGMCC No. 0584, CGMCC No. 0581, CGMCC No. 0585, CGMCC No. 0582,
10 CGMCC No. 0583, CBS 109513, DSM 14348, and CGMCC No. 0580, DSM 15064, DSM 15065, DSM 15066, DSM 15067, CGMCC No. 0747, CGMCC No. 0748, CGMCC No. 0749, and CGMCC No. 0750.

In a third embodiment, the present invention relates to polypeptides having cellobiohydrolase I activity which are encoded by nucleotide sequences which hybridize under
15 very low stringency conditions, preferably under low stringency conditions, more preferably under medium stringency conditions, more preferably under medium-high stringency conditions, even more preferably under high stringency conditions, and most preferably under very high stringency conditions with a polynucleotide probe selected from the group consisting of (i) the complementary strand of the nucleotides selected from the group consisting of:

20 nucleotides 1 to 1578 of SEQ ID NO:1,
nucleotides 1 to 1587 of SEQ ID NO:3,
nucleotides 1 to 1353 of SEQ ID NO:5,
nucleotides 1 to 1371 of SEQ ID NO:7,
nucleotides 1 to 1614 of SEQ ID NO:9,
25 nucleotides 1 to 1245 of SEQ ID NO:11,
nucleotides 1 to 1341 of SEQ ID NO:13,
nucleotides 1 to 1356 of SEQ ID NO:15,
nucleotides 1 to 1365 of SEQ ID NO:37,
nucleotides 1 to 1377 of SEQ ID NO:39,
30 nucleotides 1 to 1353 of SEQ ID NO:41,
nucleotides 1 to 1341 of SEQ ID NO:43,
nucleotides 1 to 1584 of SEQ ID NO:45,
nucleotides 1 to 1368 of SEQ ID NO:47,
nucleotides 1 to 1395 of SEQ ID NO:49,
35 nucleotides 1 to 1383 of SEQ ID NO:51,
nucleotides 1 to 1353 of SEQ ID NO:53,
nucleotides 1 to 1599 of SEQ ID NO:55,

nucleotides 1 to 1383 of SEQ ID NO:57,
nucleotides 1 to 1578 of SEQ ID NO:59, and
nucleotides 1 to 1371 of SEQ ID NO:65;

(ii) the complementary strand of the nucleotides selected from the group consisting of

- 5 nucleotides 1 to 500 of SEQ ID NO:1,
nucleotides 1 to 500 of SEQ ID NO:3,
nucleotides 1 to 500 of SEQ ID NO:5,
nucleotides 1 to 500 of SEQ ID NO:7,
nucleotides 1 to 500 of SEQ ID NO:9,
- 10 nucleotides 1 to 500 of SEQ ID NO:11,
nucleotides 1 to 500 of SEQ ID NO:13,
nucleotides 1 to 500 of SEQ ID NO:15,
nucleotides 1 to 500 of SEQ ID NO:37,
nucleotides 1 to 500 of SEQ ID NO:39,
- 15 nucleotides 1 to 500 of SEQ ID NO:41,
nucleotides 1 to 500 of SEQ ID NO:43,
nucleotides 1 to 500 of SEQ ID NO:45,
nucleotides 1 to 500 of SEQ ID NO:47,
nucleotides 1 to 500 of SEQ ID NO:49,
- 20 nucleotides 1 to 500 of SEQ ID NO:51,
nucleotides 1 to 500 of SEQ ID NO:53,
nucleotides 1 to 500 of SEQ ID NO:55,
nucleotides 1 to 500 of SEQ ID NO:57,
nucleotides 1 to 500 of SEQ ID NO:59,
- 25 nucleotides 1 to 500 of SEQ ID NO:65,
nucleotides 1 to 221 of SEQ ID NO:17,
nucleotides 1 to 239 of SEQ ID NO:18,
nucleotides 1 to 199 of SEQ ID NO:19,
nucleotides 1 to 191 of SEQ ID NO:20,
- 30 nucleotides 1 to 232 of SEQ ID NO:21,
nucleotides 1 to 467 of SEQ ID NO:22,
nucleotides 1 to 534 of SEQ ID NO:23,
nucleotides 1 to 563 of SEQ ID NO:24,
nucleotides 1 to 218 of SEQ ID NO:25,
- 35 nucleotides 1 to 492 of SEQ ID NO:26,
nucleotides 1 to 481 of SEQ ID NO:27,
nucleotides 1 to 463 of SEQ ID NO:28,

nucleotides 1 to 513 of SEQ ID NO:29,
nucleotides 1 to 579 of SEQ ID NO:30,
nucleotides 1 to 514 of SEQ ID NO:31,
nucleotides 1 to 477 of SEQ ID NO:32,
5 nucleotides 1 to 500 of SEQ ID NO:33,
nucleotides 1 to 470 of SEQ ID NO:34,
nucleotides 1 to 491 of SEQ ID NO:35,
nucleotides 1 to 221 of SEQ ID NO:36,
nucleotides 1 to 519 of SEQ ID NO:61,
10 nucleotides 1 to 497 of SEQ ID NO:62,
nucleotides 1 to 498 of SEQ ID NO:63,
nucleotides 1 to 525 of SEQ ID NO:64, and
nucleotides 1 to 951 of SEQ ID NO:67; and
(iii) the complementary strand of the nucleotides selected from the group consisting of
15 nucleotides 1 to 200 of SEQ ID NO:1,
nucleotides 1 to 200 of SEQ ID NO:3,
nucleotides 1 to 200 of SEQ ID NO:5,
nucleotides 1 to 200 of SEQ ID NO:7,
nucleotides 1 to 200 of SEQ ID NO:9,
20 nucleotides 1 to 200 of SEQ ID NO:11,
nucleotides 1 to 200 of SEQ ID NO:13,
nucleotides 1 to 200 of SEQ ID NO:15,
nucleotides 1 to 200 of SEQ ID NO:37,
nucleotides 1 to 200 of SEQ ID NO:39,
25 nucleotides 1 to 200 of SEQ ID NO:41,
nucleotides 1 to 200 of SEQ ID NO:43,
nucleotides 1 to 200 of SEQ ID NO:45,
nucleotides 1 to 200 of SEQ ID NO:47,
nucleotides 1 to 200 of SEQ ID NO:49,
30 nucleotides 1 to 200 of SEQ ID NO:51,
nucleotides 1 to 200 of SEQ ID NO:53,
nucleotides 1 to 200 of SEQ ID NO:55,
nucleotides 1 to 200 of SEQ ID NO:57,
nucleotides 1 to 200 of SEQ ID NO:59, and
35 nucleotides 1 to 200 of SEQ ID NO:65
(J. Sambrook, E.F. Fritsch, and T. Maniatus, 1989, *Molecular Cloning, A Laboratory Manual*,
2d edition, Cold Spring Harbor, New York).

In another embodiment, the present invention relates to polypeptides having cellobiohydrolase I activity which are encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in a microorganism selected from the group consisting of:

- a microorganism belonging to *Zygomycota*, preferably belonging to the *Mucorales*, more preferably belonging to the family *Mucoraceae*, most preferably belonging to the genus *Rhizomucor* (e.g. *Rhizomucor pusillus*), or the family *Choanephoraceae*, most preferably belonging to the genus *Poitrasia* (e.g. *Poitrasia circinans*),
- a microorganism belonging to the *Oomycetes*, preferably to the order *Pythiales*, more preferably to the family *Pythiaceae*, most preferably to the genus *Phytophthora* (e.g. *Phytophthora infestans*),
- a microorganism belonging to *Auriculariales* (an order of the *Basidiomycota*, *Hymenomycetes*), preferably belonging to the family *Exidiaceae*, more preferably belonging to the genus *Exidia* (e.g. *Exidia glandulosa*),
- a microorganism belonging to *Xylariales* (an order of the *Ascomycota*, *Sordariomycetes*), preferably belonging to the family *Xylariaceae*, more preferably belonging to the genus *Xylaria* (e.g. *Xylaria hypoxylon*),
- a microorganism belonging to *Dothideales* (an order of the *Ascomycota*, *Dothideomycetes*), preferably belonging to the family *Dothideaceae*, more preferably belonging to the genus *Diplodia* (e.g. *Diplodia gossypina*),
- a microorganism belonging to *Pezizales* (an order of the *Ascomycota*), preferably belonging to the family *Pyronemataceae*, more preferably belonging to the genus *Trichophaea* (e.g. *Trichophaea saccata*), or the family *Sarcosomataceae*, more preferably belonging to the genus *Pseudoplectania* (e.g. *Pseudoplectania nigrella*),
- a microorganism belonging to the family *Rigidiporaceae* (under *Basidiomycota*, *Hymenomycetes*, *Hymenomycetales*), more preferably belonging to the genus *Meripilus* (e.g. *Meripilus giganteus*),
- a microorganism belonging to the family *Meruliaceae* (under *Basidiomycota*, *Hymenomycetes*, *Sterealesales*), more preferably belonging to the genus *Sporothrichum* (*Sporothrichum* sp.),
- a microorganism belonging to the family *Agaricaceae* (under *Basidiomycota*, *Hymenomycetes*, *Agaricales*), more preferably belonging to the genus *Coprinus* (e.g. *Coprinus cinereus*),
- a microorganism belonging to the family *Hypocreaceae* (under *Ascomycota*, *Sordariomycetes*, *Hypocreales*), more preferably belonging to the genus *Acremonium* (e.g. *Acremonium thermophilum*; *Acremonium* sp.) or the (mitosporic) genus *Verticillium* (e.g. *Verticillium tenerum*),
- a microorganism belonging to the genus *Cladorrhinum* (under *Ascomycota*, *Sordariomycetes*, *Sordariales*, *Sordariaceae*) e.g. *Cladorrhinum foecundissimum*,
- a microorganism belonging to the genus *Myceliophthora* (under *Ascomycota*,

Sordariomycetes, Sordariales, Sordariaceae) e.g. *Myceliophthora thermophila* or *Myceliophthora hinnulae*,

a microorganism belonging to the genus *Chaetomium* (under *Ascomycota, Sordariomycetes, Sordariales, Chaetomiaceae*) e.g. *Chaetomium thermophilum*,

5 a microorganism belonging to the genus *Chaetomidium* (under *Ascomycota, Sordariomycetes, Sordariales, Chaetomiaceae*) e.g. *Chaetomidium pingtungium*,

a microorganism belonging to the genus *Thielavia* (under *Ascomycota, Sordariomycetes, Sordariales, Chaetomiaceae*) e.g. *Thielavia australiensis* or *Thielavia microspora*,

a microorganism belonging to the genus *Thermoascus* (under *Ascomycota, Eurotiomycetes, Eurotiales, Trichocomoaceae*) e.g. *Thermoascus aurantiacus*,

10 a microorganism belonging to the genus *Trichothecium* (mitosporic *Ascomycota*) e.g. *Trichothecium roseum*, and

a microorganism belonging to the species *Humicola nigrescens*.

A nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID
15 NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID
NO:15, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ
ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57,
SEQ ID NO:59, SEQ ID NO:65, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID
NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ
20 ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31,
SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID
NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, and SEQ ID NO:67, or a
subsequence thereof, as well as an amino acid sequence selected from the group consisting
of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12,
25 SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID
NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ
ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66, or a fragment thereof, may be
used to design a polynucleotide probe to identify and clone DNA encoding polypeptides having
cellobiohydrolase I activity from strains of different genera or species according to methods
30 well known in the art. In particular, such probes can be used for hybridization with the
genomic or cDNA of the genus or species of interest, following standard Southern blotting
procedures, in order to identify and isolate the corresponding gene therein. Such probes can
be considerably shorter than the entire sequence, but should be at least 15, preferably at least
25, more preferably at least 35 nucleotides in length, such as at least 70 nucleotides in length.
35 It is, however, preferred that the polynucleotide probe is at least 100 nucleotides in length. For
example, the polynucleotide probe may be at least 200 nucleotides in length, at least 300
nucleotides in length, at least 400 nucleotides in length or at least 500 nucleotides in length.

Even longer probes may be used, e.g., polynucleotide probes which are at least 600 nucleotides in length, at least 700 nucleotides in length, at least 800 nucleotides in length, or at least 900 nucleotides in length. Both DNA and RNA probes can be used. The probes are typically labeled for detecting the corresponding gene (for example, with ^{32}P , ^3H , ^{35}S , biotin, or avidin).

Thus, a genomic DNA or cDNA library prepared from such other organisms may be screened for DNA which hybridizes with the probes described above and which encodes a polypeptide having cellobiohydrolase I activity. Genomic or other DNA from such other organisms may be separated by agarose or polyacrylamide gel electrophoresis, or other separation techniques. DNA from the libraries or the separated DNA may be transferred to, and immobilized, on nitrocellulose or other suitable carrier materials. In order to identify a clone or DNA which is homologous with SEQ ID NO:1 the carrier material with the immobilized DNA is used in a Southern blot.

For purposes of the present invention, hybridization indicates that the nucleotide sequence hybridizes to a labeled polynucleotide probe which hybridizes to the nucleotide sequence shown in SEQ ID NO:1 under very low to very high stringency conditions. Molecules to which the polynucleotide probe hybridizes under these conditions may be detected using X-ray film or by any other method known in the art. Whenever the term "polynucleotide probe" is used in the present context, it is to be understood that such a probe contains at least 15 nucleotides.

In an interesting embodiment, the polynucleotide probe is the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 1 to 1578 of SEQ ID NO:1,
nucleotides 1 to 1302 of SEQ ID NO:1,
nucleotides 1 to 1587 of SEQ ID NO:3,
nucleotides 1 to 1302 of SEQ ID NO:3,
nucleotides 1 to 1353 of SEQ ID NO:5,
nucleotides 1 to 1302 of SEQ ID NO:5,
nucleotides 1 to 1371 of SEQ ID NO:7,
nucleotides 1 to 1302 of SEQ ID NO:7,
nucleotides 1 to 1614 of SEQ ID NO:9,
nucleotides 1 to 1302 of SEQ ID NO:9,
nucleotides 1 to 1245 of SEQ ID NO:11,
nucleotides 1 to 1341 of SEQ ID NO:13,
nucleotides 1 to 1302 of SEQ ID NO:13,
nucleotides 1 to 1356 of SEQ ID NO:15,
nucleotides 1 to 1302 of SEQ ID NO:15,

- nucleotides 1 to 1365 of SEQ ID NO:37,
nucleotides 1 to 1302 of SEQ ID NO:37,
nucleotides 1 to 1377 of SEQ ID NO:39,
nucleotides 1 to 1302 of SEQ ID NO:39,
5 nucleotides 1 to 1353 of SEQ ID NO:41,
nucleotides 1 to 1302 of SEQ ID NO:41,
nucleotides 1 to 1341 of SEQ ID NO:43,
nucleotides 1 to 1302 of SEQ ID NO:43,
nucleotides 1 to 1584 of SEQ ID NO:45,
10 nucleotides 1 to 1302 of SEQ ID NO:45,
nucleotides 1 to 1368 of SEQ ID NO:47,
nucleotides 1 to 1302 of SEQ ID NO:47,
nucleotides 1 to 1395 of SEQ ID NO:49,
nucleotides 1 to 1302 of SEQ ID NO:49,
15 nucleotides 1 to 1383 of SEQ ID NO:51,
nucleotides 1 to 1302 of SEQ ID NO:51,
nucleotides 1 to 1353 of SEQ ID NO:53,
nucleotides 1 to 1302 of SEQ ID NO:53,
nucleotides 1 to 1599 of SEQ ID NO:55,
20 nucleotides 1 to 1302 of SEQ ID NO:55,
nucleotides 1 to 1383 of SEQ ID NO:57,
nucleotides 1 to 1302 of SEQ ID NO:57,
nucleotides 1 to 1578 of SEQ ID NO:59,
nucleotides 1 to 1302 of SEQ ID NO:59,
25 nucleotides 1 to 1371 of SEQ ID NO:65, and
nucleotides 1 to 1302 of SEQ ID NO:65;
or the complementary strand of the nucleotides selected from the group consisting of:
nucleotides 1 to 500 of SEQ ID NO:1,
nucleotides 1 to 500 of SEQ ID NO:3,
30 nucleotides 1 to 500 of SEQ ID NO:5,
nucleotides 1 to 500 of SEQ ID NO:7,
nucleotides 1 to 500 of SEQ ID NO:9,
nucleotides 1 to 500 of SEQ ID NO:11,
nucleotides 1 to 500 of SEQ ID NO:13,
35 nucleotides 1 to 500 of SEQ ID NO:15,
nucleotides 1 to 500 of SEQ ID NO:37,
nucleotides 1 to 500 of SEQ ID NO:39,

nucleotides 1 to 500 of SEQ ID NO:41,
nucleotides 1 to 500 of SEQ ID NO:43,
nucleotides 1 to 500 of SEQ ID NO:45,
nucleotides 1 to 500 of SEQ ID NO:47,
5 nucleotides 1 to 500 of SEQ ID NO:49,
nucleotides 1 to 500 of SEQ ID NO:51,
nucleotides 1 to 500 of SEQ ID NO:53,
nucleotides 1 to 500 of SEQ ID NO:55,
nucleotides 1 to 500 of SEQ ID NO:57,
10 nucleotides 1 to 500 of SEQ ID NO:59,
nucleotides 1 to 500 of SEQ ID NO:65,
nucleotides 1 to 221 of SEQ ID NO:17,
nucleotides 1 to 239 of SEQ ID NO:18,
nucleotides 1 to 199 of SEQ ID NO:19,
15 nucleotides 1 to 191 of SEQ ID NO:20,
nucleotides 1 to 232 of SEQ ID NO:21,
nucleotides 1 to 467 of SEQ ID NO:22,
nucleotides 1 to 534 of SEQ ID NO:23,
nucleotides 1 to 563 of SEQ ID NO:24,
20 nucleotides 1 to 218 of SEQ ID NO:25,
nucleotides 1 to 492 of SEQ ID NO:26,
nucleotides 1 to 481 of SEQ ID NO:27,
nucleotides 1 to 463 of SEQ ID NO:28,
nucleotides 1 to 513 of SEQ ID NO:29,
25 nucleotides 1 to 579 of SEQ ID NO:30,
nucleotides 1 to 514 of SEQ ID NO:31,
nucleotides 1 to 477 of SEQ ID NO:32,
nucleotides 1 to 500 of SEQ ID NO:33,
nucleotides 1 to 470 of SEQ ID NO:34,
30 nucleotides 1 to 491 of SEQ ID NO:35,
nucleotides 1 to 221 of SEQ ID NO:36,
nucleotides 1 to 519 of SEQ ID NO:61,
nucleotides 1 to 497 of SEQ ID NO:62,
nucleotides 1 to 498 of SEQ ID NO:63,
35 nucleotides 1 to 525 of SEQ ID NO:64, and
nucleotides 1 to 951 of SEQ ID NO:67;
or the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 1 to 200 of SEQ ID NO:1,
nucleotides 1 to 200 of SEQ ID NO:3,
nucleotides 1 to 200 of SEQ ID NO:5,
nucleotides 1 to 200 of SEQ ID NO:7,
5 nucleotides 1 to 200 of SEQ ID NO:9,
nucleotides 1 to 200 of SEQ ID NO:11,
nucleotides 1 to 200 of SEQ ID NO:13,
nucleotides 1 to 200 of SEQ ID NO:15,
nucleotides 1 to 200 of SEQ ID NO:37,
10 nucleotides 1 to 200 of SEQ ID NO:39,
nucleotides 1 to 200 of SEQ ID NO:41,
nucleotides 1 to 200 of SEQ ID NO:43,
nucleotides 1 to 200 of SEQ ID NO:45,
nucleotides 1 to 200 of SEQ ID NO:47,
15 nucleotides 1 to 200 of SEQ ID NO:49,
nucleotides 1 to 200 of SEQ ID NO:51,
nucleotides 1 to 200 of SEQ ID NO:53,
nucleotides 1 to 200 of SEQ ID NO:55,
nucleotides 1 to 200 of SEQ ID NO:57,
20 nucleotides 1 to 200 of SEQ ID NO:59,
nucleotides 1 to 200 of SEQ ID NO:65,
nucleotides 1 to 200 of SEQ ID NO:22,
nucleotides 1 to 200 of SEQ ID NO:23,
nucleotides 1 to 200 of SEQ ID NO:24,
25 nucleotides 1 to 200 of SEQ ID NO:26,
nucleotides 1 to 200 of SEQ ID NO:27,
nucleotides 1 to 200 of SEQ ID NO:28,
nucleotides 1 to 200 of SEQ ID NO:29,
nucleotides 1 to 200 of SEQ ID NO:30,
30 nucleotides 1 to 200 of SEQ ID NO:31,
nucleotides 1 to 200 of SEQ ID NO:32,
nucleotides 1 to 200 of SEQ ID NO:33,
nucleotides 1 to 200 of SEQ ID NO:34,
nucleotides 1 to 200 of SEQ ID NO:35,
35 nucleotides 1 to 200 of SEQ ID NO:61,
nucleotides 1 to 200 of SEQ ID NO:62,
nucleotides 1 to 200 of SEQ ID NO:63,

nucleotides 1 to 200 of SEQ ID NO:64, and
nucleotides 1 to 200 of SEQ ID NO:67.

In another interesting embodiment, the polynucleotide probe is the complementary strand of the nucleotide sequence which encodes a polypeptide selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66. In a further interesting embodiment, the polynucleotide probe is the complementary strand of a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, and SEQ ID NO:65. In another interesting embodiment, the polynucleotide probe is the complementary strand of the nucleotide sequence contained in a plasmid which is contained in a deposited microorganism selected from the group consisting of CGMCC No. 0584, CGMCC No. 0581, CGMCC No. 0585, CGMCC No. 0582, CGMCC No. 0583, CGMCC No. 0580, CBS 109513, DSM 14348, DSM 15064, DSM 15065, DSM 15066, DSM 15067, CGMCC No. 0747, CGMCC No. 0748, CGMCC No. 0749, and CGMCC No. 0750.

For long probes of at least 100 nucleotides in length, very low to very high stringency conditions are defined as prehybridization and hybridization at 42°C in 5X SSPE, 1.0% SDS, 5X Denhardt's solution, 100 µg/ml sheared and denatured salmon sperm DNA, following standard Southern blotting procedures. Preferably, the long probes of at least 100 nucleotides do not contain more than 1000 nucleotides. For long probes of at least 100 nucleotides in length, the carrier material is finally washed three times each for 15 minutes using 2 x SSC, 0.1% SDS at 42°C (very low stringency), preferably washed three times each for 15 minutes using 0.5 x SSC, 0.1% SDS at 42°C (low stringency), more preferably washed three times each for 15 minutes using 0.2 x SSC, 0.1% SDS at 42°C (medium stringency), even more preferably washed three times each for 15 minutes using 0.2 x SSC, 0.1% SDS at 55°C (medium-high stringency), most preferably washed three times each for 15 minutes using 0.1 x SSC, 0.1% SDS at 60°C (high stringency), in particular washed three times each for 15 minutes using 0.1 x SSC, 0.1% SDS at 68°C (very high stringency).

Although not particularly preferred, it is contemplated that shorter probes, e.g. probes which are from about 15 to 99 nucleotides in length, such as from about 15 to about 70 nucleotides in length, may be also be used. For such short probes, stringency conditions are defined as prehybridization, hybridization, and washing post-hybridization at 5°C to 10°C below the calculated T_m using the calculation according to Bolton and McCarthy (1962,

Proceedings of the National Academy of Sciences USA 48:1390) in 0.9 M NaCl, 0.09 M Tris-HCl pH 7.6, 6 mM EDTA, 0.5% NP-40, 1X Denhardt's solution, 1 mM sodium pyrophosphate, 1 mM sodium monobasic phosphate, 0.1 mM ATP, and 0.2 mg of yeast RNA per ml following standard Southern blotting procedures.

- 5 For short probes which are about 15 nucleotides to 99 nucleotides in length, the carrier material is washed once in 6X SCC plus 0.1% SDS for 15 minutes and twice each for 15 minutes using 6X SSC at 5°C to 10°C below the calculated T_m .

Sources for Polypeptides Having Cellobiohydrolase I Activity

- 10 A polypeptide of the present invention may be obtained from microorganisms of any genus. For purposes of the present invention, the term "obtained from" as used herein shall mean that the polypeptide encoded by the nucleotide sequence is produced by a cell in which the nucleotide sequence is naturally present or into which the nucleotide sequence has been inserted. In a preferred embodiment, the polypeptide is secreted extracellularly.

- 15 A polypeptide of the present invention may be a bacterial polypeptide. For example, the polypeptide may be a gram positive bacterial polypeptide such as a *Bacillus* polypeptide, e.g., a *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus coagulans*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus stearothermophilus*, *Bacillus subtilis*, or *Bacillus thuringiensis* polypeptide; or a *Streptomyces* polypeptide, e.g., a *Streptomyces lividans* or *Streptomyces murinus* polypeptide; or a gram negative bacterial polypeptide, e.g., an *E. coli* or a *Pseudomonas* sp. polypeptide.

- 25 A polypeptide of the present invention may be a fungal polypeptide, and more preferably a yeast polypeptide such as a *Candida*, *Kluyveromyces*, *Neocallimastix*, *Pichia*, *Piromyces*, *Saccharomyces*, *Schizosaccharomyces*, or *Yarrowia* polypeptide; or more preferably a filamentous fungal polypeptide such as an *Acremonium*, *Aspergillus*, *Aureobasidium*, *Cryptococcus*, *Filibasidium*, *Fusarium*, *Humicola*, *Magnaporthe*, *Mucor*, *Myceliophthora*, *Neurospora*, *Paecilomyces*, *Penicillium*, *Schizophyllum*, *Talaromyces*, *Thermoascus*, *Thielavia*, *Tolypocladium*, or *Trichoderma* polypeptide.

- 30 In an interesting embodiment, the polypeptide is a *Saccharomyces carlsbergensis*, *Saccharomyces cerevisiae*, *Saccharomyces diastaticus*, *Saccharomyces douglasii*, *Saccharomyces kluyveri*, *Saccharomyces norbensis* or *Saccharomyces oviformis* polypeptide.

- In another interesting embodiment, the polypeptide is an *Aspergillus aculeatus*, *Aspergillus awamori*, *Aspergillus foetidus*, *Aspergillus japonicus*, *Aspergillus nidulans*, *Aspergillus niger*, *Aspergillus oryzae*, *Fusarium bactridioides*, *Fusarium cerealis*, *Fusarium crookwellense*, *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium graminum*, *Fusarium heterosporum*, *Fusarium negundi*, *Fusarium oxysporum*, *Fusarium reticulatum*, *Fusarium roseum*, *Fusarium sambucinum*, *Fusarium sarcochroum*, *Fusarium sporotrichioides*, *Fusarium*

sulphureum, *Fusarium torulosum*, *Fusarium trichothecioides*, *Fusarium venenatum*, *Humicola insolens*, *Humicola lanuginosa*, *Mucor miehei*, *Myceliophthora thermophila*, *Neurospora crassa*, *Penicillium purpurogenum*, *Trichoderma harzianum*, *Trichoderma koningii*, *Trichoderma longibrachiatum*, *Trichoderma reesei*, or *Trichoderma viride* polypeptide.

5 In a preferred embodiment, the polypeptide is a *Acremonium thermophilum*, *Chaetomium thermophilum*, *Scytalidium* sp., *Scytalidium thermophilum*, *Thermoascus aurantiacus*, *Thielavia australiensis*, *Verticillium tenerum*, *Neotermes castaneus*, *Melanocarpus albomyces*, *Poitrasia circinans*, *Coprinus cinereus*, *Trichothecium roseum*, *Humicola nigrescens*, *Cladorrhinum foecundissimum*, *Diplodia gossypina*, *Myceliophthora*
10 *thermophila*, *Rhizomucor pusillus*, *Meripilus giganteus*, *Exidia glandulosa*, *Xylaria hypoxylon*, *Trichophaea saccata*, *Acremonium* sp., *Chaetomium* sp., *Chaetomidium pingtungium*, *Myceliophthora thermophila*, *Myceliophthora hinnulea*, *Sporotrichum pruinosum*, *Thielavia* cf. *microspora*, *Aspergillus* sp., *Scopulariopsis* sp., *Fusarium* sp., *Verticillium* sp., *Pseudoplectania nigrella*, or *Phytophthora infestans* polypeptide.

15 In a more preferred embodiment, the polypeptide is a *Acremonium thermophilum*, *Chaetomium thermophilum*, *Scytalidium* sp., *Scytalidium thermophilum*, *Thermoascus aurantiacus*, *Thielavia australiensis*, *Verticillium tenerum*, *Neotermes castaneus*, *Melanocarpus albomyces*, *Poitrasia circinans*, or *Coprinus cinereus* polypeptide, e.g., the polypeptide consisting of an amino acid sequence selected from the group consisting of SEQ
20 ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66.

It will be understood that for the aforementioned species, the invention encompasses
25 both the perfect and imperfect states, and other taxonomic equivalents, e.g., anamorphs, regardless of the species name by which they are known. Those skilled in the art will readily recognize the identity of appropriate equivalents.

Strains of these species are readily accessible to the public in a number of culture collections, such as the American Type Culture Collection (ATCC), Deutsche Sammlung von
30 Mikroorganismen und Zellkulturen GmbH (DSMZ), China General Microbiological Culture Collection Center (CGMCC), Centraalbureau Voor Schimmelcultures (CBS), and Agricultural Research Service Patent Culture Collection, Northern Regional Research Center (NRRL).

Furthermore, such polypeptides may be identified and obtained from other sources including microorganisms isolated from nature (e.g., soil, water, plants, animals, etc.) using the
35 above-mentioned probes. Techniques for isolating microorganisms from natural habitats are well known in the art. The nucleotide sequence may then be derived by similarly screening a genomic or cDNA library of another microorganism. Once a nucleotide sequence encoding a

polypeptide has been detected with the probe(s), the sequence may be isolated or cloned by utilizing techniques which are known to those of ordinary skill in the art (see, e.g., Sambrook *et al.*, 1989, *supra*).

Polypeptides encoded by nucleotide sequences of the present invention also include
 5 fused polypeptides or cleavable fusion polypeptides in which another polypeptide is fused at the N-terminus or the C-terminus of the polypeptide or fragment thereof. A fused polypeptide is produced by fusing a nucleotide sequence (or a portion thereof) encoding another polypeptide to a nucleotide sequence (or a portion thereof) of the present invention. Techniques for producing fusion polypeptides are known in the art, and include ligating the
 10 coding sequences encoding the polypeptides so that they are in frame and that expression of the fused polypeptide is under control of the same promoter(s) and terminator.

Polynucleotides and Nucleotide Sequences

The present invention also relates to polynucleotides having a nucleotide sequence
 15 which encodes for a polypeptide of the invention. In particular, the present invention relates to polynucleotides consisting of a nucleotide sequence which encodes for a polypeptide of the invention. In a preferred embodiment, the nucleotide sequence is selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41,
 20 SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, and SEQ ID NO:65. In a more preferred embodiment, the nucleotide sequence is the mature polypeptide coding region contained in a plasmid which is contained in a deposited microorganism selected from the group consisting of CGMCC No. 0584, CGMCC No. 0581, CGMCC No. 0585, CGMCC No.
 25 0582, CGMCC No. 0583, CGMCC No. 0580, CBS 109513, DSM 14348, DSM 15064, DSM 15065, DSM 15066, DSM 15067, CGMCC No. 0747, CGMCC No. 0748, CGMCC No. 0749, and CGMCC No. 0750. The present invention also encompasses polynucleotides comprising, preferably consisting of, nucleotide sequences which encode a polypeptide consisting of an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ
 30 ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66, which differ from a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ
 35 ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, and SEQ ID NO:65 by virtue of the

degeneracy of the genetic code.

The present invention also relates to polynucleotides comprising, preferably consisting of, a subsequence of a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, and SEQ ID NO:65 which encode fragments of an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66 that have cellobiohydrolase I activity. A subsequence of a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, and SEQ ID NO:65 is a nucleotide sequence encompassed by a sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, and SEQ ID NO:65 except that one or more nucleotides from the 5' and/or 3' end have been deleted.

The present invention also relates to polynucleotides having, preferably consisting of, a modified nucleotide sequence which comprises at least one modification in the mature polypeptide coding sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, and SEQ ID NO:65, and where the modified nucleotide sequence encodes a polypeptide which consists of an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66.

The techniques used to isolate or clone a nucleotide sequence encoding a polypeptide are known in the art and include isolation from genomic DNA, preparation from cDNA, or a combination thereof. The cloning of the nucleotide sequences of the present invention from

such genomic DNA can be effected, *e.g.*, by using the well known polymerase chain reaction (PCR) or antibody screening of expression libraries to detect cloned DNA fragments with shared structural features. See, *e.g.*, Innis *et al.*, 1990, *PCR: A Guide to Methods and Application*, Academic Press, New York. Other amplification procedures such as ligase chain reaction (LCR), ligated activated transcription (LAT) and nucleotide sequence-based amplification (NASBA) may be used. The nucleotide sequence may be cloned from a strain selected from the group consisting of *Acremonium*, *Scytalidium*, *Thermoascus*, *Thielavia*, *Verticillium*, *Neotermes*, *Melanocarpus*, *Poitrasia*, *Coprinus*, *Trichothecium*, *Humicola*, *Cladorrhinum*, *Diplodia*, *Myceliophthora*, *Rhizomucor*, *Meripilus*, *Exidia*, *Xylaria*, *Trichophaea*, *Chaetomium*, *Chaetomidium*, *Sporotrichum*, *Thielavia*, *Aspergillus*, *Scopulariopsis*, *Fusarium*, *Pseudoplectania*, and *Phytophthora*, or another or related organism and thus, for example, may be an allelic or species variant of the polypeptide encoding region of the nucleotide sequence.

The nucleotide sequence may be obtained by standard cloning procedures used in genetic engineering to relocate the nucleotide sequence from its natural location to a different site where it will be reproduced. The cloning procedures may involve excision and isolation of a desired fragment comprising the nucleotide sequence encoding the polypeptide, insertion of the fragment into a vector molecule, and incorporation of the recombinant vector into a host cell where multiple copies or clones of the nucleotide sequence will be replicated. The nucleotide sequence may be of genomic, cDNA, RNA, semisynthetic, synthetic origin, or any combinations thereof.

The present invention also relates to a polynucleotide comprising, preferably consisting of, a nucleotide sequence which has a degree of identity with a nucleotide sequence selected from the group consisting of

nucleotides 1 to 1578 of SEQ ID NO:1,
 nucleotides 1 to 1587 of SEQ ID NO:3,
 nucleotides 1 to 1353 of SEQ ID NO:5,
 nucleotides 1 to 1371 of SEQ ID NO:7,
 nucleotides 1 to 1614 of SEQ ID NO:9,
 nucleotides 1 to 1245 of SEQ ID NO:11,
 nucleotides 1 to 1341 of SEQ ID NO:13,
 nucleotides 1 to 1356 of SEQ ID NO:15,
 nucleotides 1 to 1365 of SEQ ID NO:37,
 nucleotides 1 to 1377 of SEQ ID NO:39,
 nucleotides 1 to 1353 of SEQ ID NO:41,
 nucleotides 1 to 1341 of SEQ ID NO:43,
 nucleotides 1 to 1584 of SEQ ID NO:45,

nucleotides 1 to 1368 of SEQ ID NO:47,
nucleotides 1 to 1395 of SEQ ID NO:49,
nucleotides 1 to 1383 of SEQ ID NO:51,
nucleotides 1 to 1353 of SEQ ID NO:53,
5 nucleotides 1 to 1599 of SEQ ID NO:55,
nucleotides 1 to 1383 of SEQ ID NO:57,
nucleotides 1 to 1578 of SEQ ID NO:59,
nucleotides 1 to 1371 of SEQ ID NO:65,
nucleotides 1 to 500 of SEQ ID NO:1,
10 nucleotides 1 to 500 of SEQ ID NO:3,
nucleotides 1 to 500 of SEQ ID NO:5,
nucleotides 1 to 500 of SEQ ID NO:7,
nucleotides 1 to 500 of SEQ ID NO:9,
nucleotides 1 to 500 of SEQ ID NO:11,
15 nucleotides 1 to 500 of SEQ ID NO:13,
nucleotides 1 to 500 of SEQ ID NO:15,
nucleotides 1 to 500 of SEQ ID NO:37,
nucleotides 1 to 500 of SEQ ID NO:39,
nucleotides 1 to 500 of SEQ ID NO:41,
20 nucleotides 1 to 500 of SEQ ID NO:43,
nucleotides 1 to 500 of SEQ ID NO:45,
nucleotides 1 to 500 of SEQ ID NO:47,
nucleotides 1 to 500 of SEQ ID NO:49,
nucleotides 1 to 500 of SEQ ID NO:51,
25 nucleotides 1 to 500 of SEQ ID NO:53,
nucleotides 1 to 500 of SEQ ID NO:55,
nucleotides 1 to 500 of SEQ ID NO:57,
nucleotides 1 to 500 of SEQ ID NO:59,
nucleotides 1 to 500 of SEQ ID NO:65,
30 nucleotides 1 to 221 of SEQ ID NO:17,
nucleotides 1 to 239 of SEQ ID NO:18,
nucleotides 1 to 199 of SEQ ID NO:19,
nucleotides 1 to 191 of SEQ ID NO:20,
nucleotides 1 to 232 of SEQ ID NO:21,
35 nucleotides 1 to 467 of SEQ ID NO:22,
nucleotides 1 to 534 of SEQ ID NO:23,
nucleotides 1 to 563 of SEQ ID NO:24,

nucleotides 1 to 218 of SEQ ID NO:25,
 nucleotides 1 to 492 of SEQ ID NO:26,
 nucleotides 1 to 481 of SEQ ID NO:27,
 nucleotides 1 to 463 of SEQ ID NO:28,
 5 nucleotides 1 to 513 of SEQ ID NO:29,
 nucleotides 1 to 579 of SEQ ID NO:30,
 nucleotides 1 to 514 of SEQ ID NO:31,
 nucleotides 1 to 477 of SEQ ID NO:32,
 nucleotides 1 to 500 of SEQ ID NO:33,
 10 nucleotides 1 to 470 of SEQ ID NO:34,
 nucleotides 1 to 491 of SEQ ID NO:35,
 nucleotides 1 to 221 of SEQ ID NO:36,
 nucleotides 1 to 519 of SEQ ID NO:61,
 nucleotides 1 to 497 of SEQ ID NO:62,
 15 nucleotides 1 to 498 of SEQ ID NO:63,
 nucleotides 1 to 525 of SEQ ID NO:64, and
 nucleotides 1 to 951 of SEQ ID NO:67

of at least 70% identity, such as at least 75% identity; preferably, the nucleotide sequence has at least 80% identity, e.g. at least 85% identity, such as at least 90% identity, more preferably at least 95% identity, such as at least 96% identity, e.g. at least 97% identity, even more preferably at least 98% identity, such as at least 99%. Preferably, the nucleotide sequence encodes a polypeptide having cellobiohydrolase I activity. The degree of identity between two nucleotide sequences is determined as described previously (see the section entitled "Definitions").

25 In another interesting aspect, the present invention relates to a polynucleotide having, preferably consisting of, a nucleotide sequence which has at least 65% identity with the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in a deposited microorganism selected from the group consisting of CGMCC No. 0584, CGMCC No. 0581, CGMCC No. 0585, CGMCC No. 0582, CGMCC No. 0583, CGMCC No. 0580, CBS
 30 109513, DSM 14348, DSM 15064, DSM 15065, DSM 15066, DSM 15067, CGMCC No. 0747, CGMCC No. 0748, CGMCC No. 0749, and CGMCC No. 0750. In a preferred embodiment, the degree of identity with the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in a deposited microorganism selected from the group consisting of CGMCC No. 0584, CGMCC No. 0581, CGMCC No. 0585, CGMCC No. 0582, CGMCC No. 0583, CGMCC No. 0580, CBS 109513, DSM 14348, DSM 15064, DSM 15065,
 35 DSM 15066, DSM 15067, CGMCC No. 0747, CGMCC No. 0748, CGMCC No. 0749, and CGMCC No. 0750 is at least 70%, e.g. at least 80%, such as at least 90%, more preferably at

least 95%, such as at least 96%, e.g. at least 97%, even more preferably at least 98%, such as at least 99%. Preferably, the nucleotide sequence comprises the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in a deposited microorganism selected from the group consisting of CGMCC No. 0584, CGMCC No. 0581, CGMCC No. 0585, CGMCC No. 0582, CGMCC No. 0583, CGMCC No. 0580, CBS 109513, DSM 14348, DSM 15064, DSM 15065, DSM 15066, DSM 15067, CGMCC No. 0747, CGMCC No. 0748, CGMCC No. 0749, and CGMCC No. 0750. In an even more preferred embodiment, the nucleotide sequence consists of the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in a deposited microorganism selected from the group consisting of CGMCC No. 0584, CGMCC No. 0581, CGMCC No. 0585, CGMCC No. 0582, CGMCC No. 0583, CGMCC No. 0580, CBS 109513, DSM 14348, DSM 15064, DSM 15065, DSM 15066, DSM 15067, CGMCC No. 0747, CGMCC No. 0748, CGMCC No. 0749, and CGMCC No. 0750.

Modification of a nucleotide sequence encoding a polypeptide of the present invention may be necessary for the synthesis of a polypeptide, which comprises an amino acid sequence that has at least one substitution, deletion and/or insertion as compared to an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, and SEQ ID NO:66. These artificial variants may differ in some engineered way from the polypeptide isolated from its native source, e.g., variants that differ in specific activity, thermostability, pH optimum, or the like.

It will be apparent to those skilled in the art that such modifications can be made outside the regions critical to the function of the molecule and still result in an active polypeptide. Amino acid residues essential to the activity of the polypeptide encoded by the nucleotide sequence of the invention, and therefore preferably not subject to modification, such as substitution, may be identified according to procedures known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (see, e.g., Cunningham and Wells, 1989, *Science* 244: 1081-1085). In the latter technique, mutations are introduced at every positively charged residue in the molecule, and the resultant mutant molecules are tested for cellobiohydrolase I activity to identify amino acid residues that are critical to the activity of the molecule. Sites of substrate-enzyme interaction can also be determined by analysis of the three-dimensional structure as determined by such techniques as nuclear magnetic resonance analysis, crystallography or photoaffinity labelling (see, e.g., de Vos *et al.*, 1992, *Science* 255: 306-312; Smith *et al.*, 1992, *Journal of Molecular Biology* 224: 899-904; Wlodaver *et al.*, 1992, *FEBS Letters* 309: 59-64).

Moreover, a nucleotide sequence encoding a polypeptide of the present invention may be modified by introduction of nucleotide substitutions which do not give rise to another amino acid sequence of the polypeptide encoded by the nucleotide sequence, but which correspond to the codon usage of the host organism intended for production of the enzyme.

5 The introduction of a mutation into the nucleotide sequence to exchange one nucleotide for another nucleotide may be accomplished by site-directed mutagenesis using any of the methods known in the art. Particularly useful is the procedure, which utilizes a supercoiled, double stranded DNA vector with an insert of interest and two synthetic primers containing the desired mutation. The oligonucleotide primers, each complementary to opposite strands of
10 the vector, extend during temperature cycling by means of *Pfu* DNA polymerase. On incorporation of the primers, a mutated plasmid containing staggered nicks is generated. Following temperature cycling, the product is treated with *DpnI* which is specific for methylated and hemimethylated DNA to digest the parental DNA template and to select for mutation-containing synthesized DNA. Other procedures known in the art may also be used. For a
15 general description of nucleotide substitution, see, e.g., Ford *et al.*, 1991, *Protein Expression and Purification* 2: 95-107.

The present invention also relates to a polynucleotide comprising, preferably consisting of, a nucleotide sequence which encodes a polypeptide having cellobiohydrolase I activity, and which hybridizes under very low stringency conditions, preferably under low stringency
20 conditions, more preferably under medium stringency conditions, more preferably under medium-high stringency conditions, even more preferably under high stringency conditions, and most preferably under very high stringency conditions with a polynucleotide probe selected from the group consisting of

(i) the complementary strand of the nucleotides selected from the group consisting of:

25 nucleotides 1 to 1578 of SEQ ID NO:1,
nucleotides 1 to 1302 of SEQ ID NO:1,
nucleotides 1 to 1587 of SEQ ID NO:3,
nucleotides 1 to 1302 of SEQ ID NO:3,
nucleotides 1 to 1353 of SEQ ID NO:5,
30 nucleotides 1 to 1302 of SEQ ID NO:5,
nucleotides 1 to 1371 of SEQ ID NO:7,
nucleotides 1 to 1302 of SEQ ID NO:7,
nucleotides 1 to 1614 of SEQ ID NO:9,
nucleotides 1 to 1302 of SEQ ID NO:9,
35 nucleotides 1 to 1245 of SEQ ID NO:11,
nucleotides 1 to 1341 of SEQ ID NO:13,
nucleotides 1 to 1302 of SEQ ID NO:13,

- nucleotides 1 to 1356 of SEQ ID NO:15,
 nucleotides 1 to 1302 of SEQ ID NO:15,
 nucleotides 1 to 1365 of SEQ ID NO:37,
 nucleotides 1 to 1302 of SEQ ID NO:37,
 5 nucleotides 1 to 1377 of SEQ ID NO:39,
 nucleotides 1 to 1302 of SEQ ID NO:39,
 nucleotides 1 to 1353 of SEQ ID NO:41,
 nucleotides 1 to 1302 of SEQ ID NO:41,
 nucleotides 1 to 1341 of SEQ ID NO:43,
 10 nucleotides 1 to 1302 of SEQ ID NO:43,
 nucleotides 1 to 1584 of SEQ ID NO:45,
 nucleotides 1 to 1302 of SEQ ID NO:45,
 nucleotides 1 to 1368 of SEQ ID NO:47,
 nucleotides 1 to 1302 of SEQ ID NO:47,
 15 nucleotides 1 to 1395 of SEQ ID NO:49,
 nucleotides 1 to 1302 of SEQ ID NO:49,
 nucleotides 1 to 1383 of SEQ ID NO:51,
 nucleotides 1 to 1302 of SEQ ID NO:51,
 nucleotides 1 to 1353 of SEQ ID NO:53,
 20 nucleotides 1 to 1302 of SEQ ID NO:53,
 nucleotides 1 to 1599 of SEQ ID NO:55,
 nucleotides 1 to 1302 of SEQ ID NO:55,
 nucleotides 1 to 1383 of SEQ ID NO:57,
 nucleotides 1 to 1302 of SEQ ID NO:57,
 25 nucleotides 1 to 1578 of SEQ ID NO:59,
 nucleotides 1 to 1302 of SEQ ID NO:59,
 nucleotides 1 to 1371 of SEQ ID NO:65, and
 nucleotides 1 to 1302 of SEQ ID NO:65;
- (ii) the complementary strand of the nucleotides selected from the group consisting of:
- 30 nucleotides 1 to 500 of SEQ ID NO:1,
 nucleotides 1 to 500 of SEQ ID NO:3,
 nucleotides 1 to 500 of SEQ ID NO:5,
 nucleotides 1 to 500 of SEQ ID NO:7,
 nucleotides 1 to 500 of SEQ ID NO:9,
 35 nucleotides 1 to 500 of SEQ ID NO:11,
 nucleotides 1 to 500 of SEQ ID NO:13,
 nucleotides 1 to 500 of SEQ ID NO:15,

nucleotides 1 to 500 of SEQ ID NO:37,
nucleotides 1 to 500 of SEQ ID NO:39,
nucleotides 1 to 500 of SEQ ID NO:41,
nucleotides 1 to 500 of SEQ ID NO:43,
5 nucleotides 1 to 500 of SEQ ID NO:45,
nucleotides 1 to 500 of SEQ ID NO:47,
nucleotides 1 to 500 of SEQ ID NO:49,
nucleotides 1 to 500 of SEQ ID NO:51,
nucleotides 1 to 500 of SEQ ID NO:53,
10 nucleotides 1 to 500 of SEQ ID NO:55,
nucleotides 1 to 500 of SEQ ID NO:57,
nucleotides 1 to 500 of SEQ ID NO:59,
nucleotides 1 to 500 of SEQ ID NO:65,
nucleotides 1 to 221 of SEQ ID NO:17,
15 nucleotides 1 to 239 of SEQ ID NO:18,
nucleotides 1 to 199 of SEQ ID NO:19,
nucleotides 1 to 191 of SEQ ID NO:20,
nucleotides 1 to 232 of SEQ ID NO:21,
nucleotides 1 to 467 of SEQ ID NO:22,
20 nucleotides 1 to 534 of SEQ ID NO:23,
nucleotides 1 to 563 of SEQ ID NO:24,
nucleotides 1 to 218 of SEQ ID NO:25,
nucleotides 1 to 492 of SEQ ID NO:26,
nucleotides 1 to 481 of SEQ ID NO:27,
25 nucleotides 1 to 463 of SEQ ID NO:28,
nucleotides 1 to 513 of SEQ ID NO:29,
nucleotides 1 to 579 of SEQ ID NO:30,
nucleotides 1 to 514 of SEQ ID NO:31,
nucleotides 1 to 477 of SEQ ID NO:32,
30 nucleotides 1 to 500 of SEQ ID NO:33,
nucleotides 1 to 470 of SEQ ID NO:34,
nucleotides 1 to 491 of SEQ ID NO:35,
nucleotides 1 to 221 of SEQ ID NO:36,
nucleotides 1 to 519 of SEQ ID NO:61,
35 nucleotides 1 to 497 of SEQ ID NO:62,
nucleotides 1 to 498 of SEQ ID NO:63,
nucleotides 1 to 525 of SEQ ID NO:64, and

nucleotides 1 to 951 of SEQ ID NO:67; and

(iii) the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 1 to 200 of SEQ ID NO:1,

nucleotides 1 to 200 of SEQ ID NO:3,

5 nucleotides 1 to 200 of SEQ ID NO:5,

nucleotides 1 to 200 of SEQ ID NO:7,

nucleotides 1 to 200 of SEQ ID NO:9,

nucleotides 1 to 200 of SEQ ID NO:11,

nucleotides 1 to 200 of SEQ ID NO:13,

10 nucleotides 1 to 200 of SEQ ID NO:15,

nucleotides 1 to 200 of SEQ ID NO:37,

nucleotides 1 to 200 of SEQ ID NO:39,

nucleotides 1 to 200 of SEQ ID NO:41,

nucleotides 1 to 200 of SEQ ID NO:43,

15 nucleotides 1 to 200 of SEQ ID NO:45,

nucleotides 1 to 200 of SEQ ID NO:47,

nucleotides 1 to 200 of SEQ ID NO:49,

nucleotides 1 to 200 of SEQ ID NO:51,

nucleotides 1 to 200 of SEQ ID NO:53,

20 nucleotides 1 to 200 of SEQ ID NO:55,

nucleotides 1 to 200 of SEQ ID NO:57,

nucleotides 1 to 200 of SEQ ID NO:59,

nucleotides 1 to 200 of SEQ ID NO:65,

nucleotides 1 to 200 of SEQ ID NO:22,

25 nucleotides 1 to 200 of SEQ ID NO:23,

nucleotides 1 to 200 of SEQ ID NO:24,

nucleotides 1 to 200 of SEQ ID NO:26,

nucleotides 1 to 200 of SEQ ID NO:27,

nucleotides 1 to 200 of SEQ ID NO:28,

30 nucleotides 1 to 200 of SEQ ID NO:29,

nucleotides 1 to 200 of SEQ ID NO:30,

nucleotides 1 to 200 of SEQ ID NO:31,

nucleotides 1 to 200 of SEQ ID NO:32,

nucleotides 1 to 200 of SEQ ID NO:33,

35 nucleotides 1 to 200 of SEQ ID NO:34,

nucleotides 1 to 200 of SEQ ID NO:35,

nucleotides 1 to 200 of SEQ ID NO:61,

nucleotides 1 to 200 of SEQ ID NO:62,
nucleotides 1 to 200 of SEQ ID NO:63,
nucleotides 1 to 200 of SEQ ID NO:64, and
nucleotides 1 to 200 of SEQ ID NO:67.

- 5 As will be understood, details and particulars concerning hybridization of the nucleotide sequences will be the same or analogous to the hybridization aspects discussed in the section entitled "Polypeptides Having Cellobiohydrolase I Activity" herein.

Nucleic Acid Constructs

- 10 The present invention also relates to nucleic acid constructs comprising a nucleotide sequence of the present invention operably linked to one or more control sequences that direct the expression of the coding sequence in a suitable host cell under conditions compatible with the control sequences.

- 15 A nucleotide sequence encoding a polypeptide of the present invention may be manipulated in a variety of ways to provide for expression of the polypeptide. Manipulation of the nucleotide sequence prior to its insertion into a vector may be desirable or necessary depending on the expression vector. The techniques for modifying nucleotide sequences utilizing recombinant DNA methods are well known in the art.

- 20 The control sequence may be an appropriate promoter sequence, a nucleotide sequence which is recognized by a host cell for expression of the nucleotide sequence. The promoter sequence contains transcriptional control sequences, which mediate the expression of the polypeptide. The promoter may be any nucleotide sequence which shows transcriptional activity in the host cell of choice including mutant, truncated, and hybrid promoters, and may be obtained from genes encoding extracellular or intracellular
25 polypeptides either homologous or heterologous to the host cell.

- Examples of suitable promoters for directing the transcription of the nucleic acid constructs of the present invention, especially in a bacterial host cell, are the promoters obtained from the *E. coli lac* operon, *Streptomyces coelicolor* agarase gene (*dagA*), *Bacillus subtilis* levansucrase gene (*sacB*), *Bacillus licheniformis* alpha-amylase gene (*amyL*), *Bacillus*
30 *stearothermophilus* maltogenic amylase gene (*amyM*), *Bacillus amyloliquefaciens* alpha-amylase gene (*amyQ*), *Bacillus licheniformis* penicillinase gene (*penP*), *Bacillus subtilis* *xylA* and *xylB* genes, and prokaryotic beta-lactamase gene (Villa-Kamaroff *et al.*, 1978, *Proceedings of the National Academy of Sciences USA* 75: 3727-3731), as well as the *tac* promoter (DeBoer *et al.*, 1983, *Proceedings of the National Academy of Sciences USA* 80: 21-
35 25). Further promoters are described in "Useful proteins from recombinant bacteria" in *Scientific American*, 1980, 242: 74-94; and in Sambrook *et al.*, 1989, *supra*.

Examples of suitable promoters for directing the transcription of the nucleic acid

constructs of the present invention in a filamentous fungal host cell are promoters obtained from the genes for *Aspergillus oryzae* TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *Aspergillus niger* neutral alpha-amylase, *Aspergillus niger* acid stable alpha-amylase, *Aspergillus niger* or *Aspergillus awamori* glucoamylase (*glaA*), *Rhizomucor miehei* lipase, *Aspergillus oryzae* alkaline protease, *Aspergillus oryzae* triose phosphate isomerase, *Aspergillus nidulans* acetamidase, and *Fusarium oxysporum* trypsin-like protease (WO 96/00787), as well as the NA2-tpi promoter (a hybrid of the promoters from the genes for *Aspergillus niger* neutral alpha-amylase and *Aspergillus oryzae* triose phosphate isomerase), and mutant, truncated, and hybrid promoters thereof.

In a yeast host, useful promoters are obtained from the genes for *Saccharomyces cerevisiae* enolase (ENO-1), *Saccharomyces cerevisiae* galactokinase (GAL1), *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH2/GAP), and *Saccharomyces cerevisiae* 3-phosphoglycerate kinase. Other useful promoters for yeast host cells are described by Romanos *et al.*, 1992, *Yeast* 8: 423-488.

The control sequence may also be a suitable transcription terminator sequence, a sequence recognized by a host cell to terminate transcription. The terminator sequence is operably linked to the 3' terminus of the nucleotide sequence encoding the polypeptide. Any terminator which is functional in the host cell of choice may be used in the present invention.

Preferred terminators for filamentous fungal host cells are obtained from the genes for *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* glucoamylase, *Aspergillus nidulans* anthranilate synthase, *Aspergillus niger* alpha-glucosidase, and *Fusarium oxysporum* trypsin-like protease.

Preferred terminators for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* enolase, *Saccharomyces cerevisiae* cytochrome C (CYC1), and *Saccharomyces cerevisiae* glyceraldehyde-3-phosphate dehydrogenase. Other useful terminators for yeast host cells are described by Romanos *et al.*, 1992, *supra*.

The control sequence may also be a suitable leader sequence, a nontranslated region of an mRNA which is important for translation by the host cell. The leader sequence is operably linked to the 5' terminus of the nucleotide sequence encoding the polypeptide. Any leader sequence that is functional in the host cell of choice may be used in the present invention.

Preferred leaders for filamentous fungal host cells are obtained from the genes for *Aspergillus oryzae* TAKA amylase and *Aspergillus nidulans* triose phosphate isomerase.

Suitable leaders for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* enolase (ENO-1), *Saccharomyces cerevisiae* 3-phosphoglycerate kinase, *Saccharomyces cerevisiae* alpha-factor, and *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH2/GAP).

The control sequence may also be a polyadenylation sequence, a sequence operably linked to the 3' terminus of the nucleotide sequence and which, when transcribed, is recognized by the host cell as a signal to add polyadenosine residues to transcribed mRNA. Any polyadenylation sequence which is functional in the host cell of choice may be used in the present invention.

Preferred polyadenylation sequences for filamentous fungal host cells are obtained from the genes for *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* glucoamylase, *Aspergillus nidulans* anthranilate synthase, *Fusarium oxysporum* trypsin-like protease, and *Aspergillus niger* alpha-glucosidase.

Useful polyadenylation sequences for yeast host cells are described by Guo and Sherman, 1995, *Molecular Cellular Biology* 15: 5983-5990.

The control sequence may also be a signal peptide coding region that codes for an amino acid sequence linked to the amino terminus of a polypeptide and directs the encoded polypeptide into the cell's secretory pathway. The 5' end of the coding sequence of the nucleotide sequence may inherently contain a signal peptide coding region naturally linked in translation reading frame with the segment of the coding region which encodes the secreted polypeptide. Alternatively, the 5' end of the coding sequence may contain a signal peptide coding region which is foreign to the coding sequence. The foreign signal peptide coding region may be required where the coding sequence does not naturally contain a signal peptide coding region. Alternatively, the foreign signal peptide coding region may simply replace the natural signal peptide coding region in order to enhance secretion of the polypeptide. However, any signal peptide coding region which directs the expressed polypeptide into the secretory pathway of a host cell of choice may be used in the present invention.

Effective signal peptide coding regions for bacterial host cells are the signal peptide coding regions obtained from the genes for *Bacillus* NCIB 11837 maltogenic amylase, *Bacillus stearothermophilus* alpha-amylase, *Bacillus licheniformis* subtilisin, *Bacillus licheniformis* beta-lactamase, *Bacillus stearothermophilus* neutral proteases (*nprT*, *nprS*, *nprM*), and *Bacillus subtilis* *prsA*. Further signal peptides are described by Simonen and Palva, 1993, *Microbiological Reviews* 57: 109-137.

Effective signal peptide coding regions for filamentous fungal host cells are the signal peptide coding regions obtained from the genes for *Aspergillus oryzae* TAKA amylase, *Aspergillus niger* neutral amylase, *Aspergillus niger* glucoamylase, *Rhizomucor miehei* aspartic proteinase, *Humicola insolens* cellulase, and *Humicola lanuginosa* lipase.

Useful signal peptides for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* alpha-factor and *Saccharomyces cerevisiae* invertase. Other useful signal peptide coding regions are described by Romanos *et al.*, 1992, *supra*.

The control sequence may also be a propeptide coding region that codes for an amino

acid sequence positioned at the amino terminus of a polypeptide. The resultant polypeptide is known as a proenzyme or propolypeptide (or a zymogen in some cases). A propolypeptide is generally inactive and can be converted to a mature active polypeptide by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide. The propeptide coding region may be obtained from the genes for *Bacillus subtilis* alkaline protease (*aprE*), *Bacillus subtilis* neutral protease (*nprT*), *Saccharomyces cerevisiae* alpha-factor, *Rhizomucor miehei* aspartic proteinase, and *Myceliophthora thermophila* laccase (WO 95/33836).

Where both signal peptide and propeptide regions are present at the amino terminus of a polypeptide, the propeptide region is positioned next to the amino terminus of a polypeptide and the signal peptide region is positioned next to the amino terminus of the propeptide region.

It may also be desirable to add regulatory sequences which allow the regulation of the expression of the polypeptide relative to the growth of the host cell. Examples of regulatory systems are those which cause the expression of the gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Regulatory systems in prokaryotic systems include the *lac*, *tac*, and *trp* operator systems. In yeast, the ADH2 system or GAL1 system may be used. In filamentous fungi, the TAKA alpha-amylase promoter, *Aspergillus niger* glucoamylase promoter, and *Aspergillus oryzae* glucoamylase promoter may be used as regulatory sequences. Other examples of regulatory sequences are those which allow for gene amplification. In eukaryotic systems, these include the dihydrofolate reductase gene which is amplified in the presence of methotrexate, and the metallothionein genes which are amplified with heavy metals. In these cases, the nucleotide sequence encoding the polypeptide would be operably linked with the regulatory sequence.

Expression Vectors

The present invention also relates to recombinant expression vectors comprising the nucleic acid construct of the invention. The various nucleotide and control sequences described above may be joined together to produce a recombinant expression vector which may include one or more convenient restriction sites to allow for insertion or substitution of the nucleotide sequence encoding the polypeptide at such sites. Alternatively, the nucleotide sequence of the present invention may be expressed by inserting the nucleotide sequence or a nucleic acid construct comprising the sequence into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression.

The recombinant expression vector may be any vector (e.g., a plasmid or virus) which can be conveniently subjected to recombinant DNA procedures and can bring about the expression of the nucleotide sequence. The choice of the vector will typically depend on the

compatibility of the vector with the host cell into which the vector is to be introduced. The vectors may be linear or closed circular plasmids.

The vector may be an autonomously replicating vector, *i.e.*, a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome.

The vector may contain any means for assuring self-replication. Alternatively, the vector may be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. Furthermore, a single vector or plasmid or two or more vectors or plasmids which together contain the total DNA to be introduced into the genome of the host cell, or a transposon may be used.

The vectors of the present invention preferably contain one or more selectable markers which permit easy selection of transformed cells. A selectable marker is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like.

Examples of bacterial selectable markers are the *dal* genes from *Bacillus subtilis* or *Bacillus licheniformis*, or markers which confer antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracycline resistance. Suitable markers for yeast host cells are ADE2, HIS3, LEU2, LYS2, MET3, TRP1, and URA3. Selectable markers for use in a filamentous fungal host cell include, but are not limited to, *amdS* (acetamidase), *argB* (ornithine carbamoyltransferase), *bar* (phosphinothricin acetyltransferase), *hygB* (hygromycin phosphotransferase), *niaD* (nitrate reductase), *pyrG* (orotidine-5'-phosphate decarboxylase), *sC* (sulfate adenylyltransferase), *trpC* (anthranilate synthase), as well as equivalents thereof.

Preferred for use in an *Aspergillus* cell are the *amdS* and *pyrG* genes of *Aspergillus nidulans* or *Aspergillus oryzae* and the *bar* gene of *Streptomyces hygrosopicus*.

The vectors of the present invention preferably contain an element(s) that permits stable integration of the vector into the host cell's genome or autonomous replication of the vector in the cell independent of the genome.

For integration into the host cell genome, the vector may rely on the nucleotide sequence encoding the polypeptide or any other element of the vector for stable integration of the vector into the genome by homologous or nonhomologous recombination. Alternatively, the vector may contain additional nucleotide sequences for directing integration by homologous recombination into the genome of the host cell. The additional nucleotide sequences enable the vector to be integrated into the host cell genome at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, the integrational elements should preferably contain a sufficient number of nucleotides, such as 100 to 1,500 base pairs, preferably 400 to 1,500 base pairs, and most preferably 800 to 1,500

base pairs, which are highly homologous with the corresponding target sequence to enhance the probability of homologous recombination. The integrational elements may be any sequence that is homologous with the target sequence in the genome of the host cell. Furthermore, the integrational elements may be non-encoding or encoding nucleotide sequences. On the other hand, the vector may be integrated into the genome of the host cell by non-homologous recombination.

For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. Examples of bacterial origins of replication are the origins of replication of plasmids pBR322, pUC19, pACYC177, and pACYC184 permitting replication in *E. coli*, and pUB110, pE194, pTA1060, and pAM β 1 permitting replication in *Bacillus*. Examples of origins of replication for use in a yeast host cell are the 2 micron origin of replication, ARS1, ARS4, the combination of ARS1 and CEN3, and the combination of ARS4 and CEN6. The origin of replication may be one having a mutation which makes its functioning temperature-sensitive in the host cell (see, e.g., Ehrlich, 1978, *Proceedings of the National Academy of Sciences USA* 75: 1433).

More than one copy of a nucleotide sequence of the present invention may be inserted into the host cell to increase production of the gene product. An increase in the copy number of the nucleotide sequence can be obtained by integrating at least one additional copy of the sequence into the host cell genome or by including an amplifiable selectable marker gene with the nucleotide sequence where cells containing amplified copies of the selectable marker gene, and thereby additional copies of the nucleotide sequence, can be selected for by cultivating the cells in the presence of the appropriate selectable agent.

The procedures used to ligate the elements described above to construct the recombinant expression vectors of the present invention are well known to one skilled in the art (see, e.g., Sambrook *et al.*, 1989, *supra*).

Host Cells

The present invention also relates to recombinant a host cell comprising the nucleic acid construct of the invention, which are advantageously used in the recombinant production of the polypeptides. A vector comprising a nucleotide sequence of the present invention is introduced into a host cell so that the vector is maintained as a chromosomal integrant or as a self-replicating extra-chromosomal vector as described earlier.

The host cell may be a unicellular microorganism, e.g., a prokaryote, or a non-unicellular microorganism, e.g., a eukaryote.

Useful unicellular cells are bacterial cells such as gram positive bacteria including, but not limited to, a *Bacillus* cell, e.g., *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus lautus*, *Bacillus lentus*,

Bacillus licheniformis, *Bacillus megaterium*, *Bacillus stearothermophilus*, *Bacillus subtilis*, and *Bacillus thuringiensis*; or a *Streptomyces* cell, e.g., *Streptomyces lividans* or *Streptomyces murinus*, or gram negative bacteria such as *E. coli* and *Pseudomonas* sp. In a preferred embodiment, the bacterial host cell is a *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus stearothermophilus*, or *Bacillus subtilis* cell. In another preferred embodiment, the *Bacillus* cell is an alkalophilic *Bacillus*.

The introduction of a vector into a bacterial host cell may, for instance, be effected by protoplast transformation (see, e.g., Chang and Cohen, 1979, *Molecular General Genetics* 168: 111-115), using competent cells (see, e.g., Young and Spizizin, 1961, *Journal of Bacteriology* 81: 823-829, or Dubnau and Davidoff-Abelson, 1971, *Journal of Molecular Biology* 56: 209-221), electroporation (see, e.g., Shigekawa and Dower, 1988, *Biotechniques* 6: 742-751), or conjugation (see, e.g., Koehler and Thorne, 1987, *Journal of Bacteriology* 169: 5771-5278).

The host cell may be a eukaryote, such as a mammalian, insect, plant, or fungal cell.

In a preferred embodiment, the host cell is a fungal cell. "Fungi" as used herein includes the phyla Ascomycota, Basidiomycota, Chytridiomycota, and Zygomycota (as defined by Hawksworth *et al.*, In, *Ainsworth and Bisby's Dictionary of The Fungi*, 8th edition, 1995, CAB International, University Press, Cambridge, UK) as well as the Oomycota (as cited in Hawksworth *et al.*, 1995, *supra*, page 171) and all mitosporic fungi (Hawksworth *et al.*, 1995, *supra*).

In a more preferred embodiment, the fungal host cell is a yeast cell. "Yeast" as used herein includes ascosporeogenous yeast (Endomycetales), basidiosporeogenous yeast, and yeast belonging to the Fungi Imperfecti (Blastomycetes). Since the classification of yeast may change in the future, for the purposes of this invention, yeast shall be defined as described in *Biology and Activities of Yeast* (Skinner, F.A., Passmore, S.M., and Davenport, R.R., eds, Soc. App. Bacteriol. Symposium Series No. 9, 1980).

In an even more preferred embodiment, the yeast host cell is a *Candida*, *Aschbyii*, *Hansenula*, *Kluyveromyces*, *Pichia*, *Saccharomyces*, *Schizosaccharomyces*, or *Yarrowia* cell.

In a most preferred embodiment, the yeast host cell is a *Saccharomyces carlsbergensis*, *Saccharomyces cerevisiae*, *Saccharomyces diastaticus*, *Saccharomyces douglasii*, *Saccharomyces kluyveri*, *Saccharomyces norbensis* or *Saccharomyces oviformis* cell. In another most preferred embodiment, the yeast host cell is a *Kluyveromyces lactis* cell. In another most preferred embodiment, the yeast host cell is a *Yarrowia lipolytica* cell.

In another more preferred embodiment, the fungal host cell is a filamentous fungal cell. "Filamentous fungi" include all filamentous forms of the subdivision Eumycota and Oomycota (as defined by Hawksworth *et al.*, 1995, *supra*). The filamentous fungi are characterized by a mycelial wall composed of chitin, cellulose, glucan, chitosan, mannan, and other complex

polysaccharides. Vegetative growth is by hyphal elongation and carbon catabolism is obligately aerobic. In contrast, vegetative growth by yeasts such as *Saccharomyces cerevisiae* is by budding of a unicellular thallus and carbon catabolism may be fermentative.

In an even more preferred embodiment, the filamentous fungal host cell is a cell of a species of, but not limited to, *Acremonium*, *Aspergillus*, *Fusarium*, *Humicola*, *Mucor*, *Myceliophthora*, *Neurospora*, *Penicillium*, *Thielavia*, *Tolypocladium*, or *Trichoderma*.

In a most preferred embodiment, the filamentous fungal host cell is an *Aspergillus awamori*, *Aspergillus foetidus*, *Aspergillus japonicus*, *Aspergillus nidulans*, *Aspergillus niger* or *Aspergillus oryzae* cell. In another most preferred embodiment, the filamentous fungal host

cell is a *Fusarium bactridioides*, *Fusarium cerealis*, *Fusarium crookwellense*, *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium graminum*, *Fusarium heterosporum*, *Fusarium negundi*, *Fusarium oxysporum*, *Fusarium reticulatum*, *Fusarium roseum*, *Fusarium sambucinum*, *Fusarium sarcochroum*, *Fusarium sporotrichioides*, *Fusarium sulphureum*, *Fusarium torulosum*, *Fusarium trichothecioides*, or *Fusarium venenatum* cell. In an even most

preferred embodiment, the filamentous fungal parent cell is a *Fusarium venenatum* (Nirenberg sp. nov.) cell. In another most preferred embodiment, the filamentous fungal host cell is a *Humicola insolens*, *Humicola lanuginosa*, *Mucor miehei*, *Myceliophthora thermophila*, *Neurospora crassa*, *Penicillium purpurogenum*, *Thielavia terrestris*, *Trichoderma harzianum*, *Trichoderma koningii*, *Trichoderma longibrachiatum*, *Trichoderma reesei*, or *Trichoderma viride* cell.

Fungal cells may be transformed by a process involving protoplast formation, transformation of the protoplasts, and regeneration of the cell wall in a manner known *per se*. Suitable procedures for transformation of *Aspergillus* host cells are described in EP 238 023 and Yelton *et al.*, 1984, *Proceedings of the National Academy of Sciences USA* 81: 1470-1474. Suitable methods for transforming *Fusarium* species are described by Malardier *et al.*, 1989, *Gene* 78: 147-156 and WO 96/00787. Yeast may be transformed using the procedures described by Becker and Guarente, *In* Abelson, J.N. and Simon, M.I., editors, *Guide to Yeast Genetics and Molecular Biology, Methods in Enzymology*, Volume 194, pp 182-187, Academic Press, Inc., New York; Ito *et al.*, 1983, *Journal of Bacteriology* 153: 163; and Hinnen *et al.*, 1978, *Proceedings of the National Academy of Sciences USA* 75: 1920.

Methods of Production

The present invention also relates to methods for producing a polypeptide of the present invention comprising (a) cultivating a strain, which in its wild-type form is capable of producing the polypeptide; and (b) recovering the polypeptide. Preferably, the strain is selected from the group consisting of *Acremonium*, *Scytalidium*, *Thermoascus*, *Thielavia*, *Verticillium*, *Neotermes*, *Melanocarpus*, *Poitrasia*, *Coprinus*, *Trichothecium*, *Humicola*, *Cladorrhinum*,

Diplodia, *Myceliophthora*, *Rhizomucor*, *Meripilus*, *Exidia*, *Xylaria*, *Trichophaea*, *Chaetomium*, *Chaetomidium*, *Sporotrichum*, *Thielavia*, *Aspergillus*, *Scopulariopsis*, *Fusarium*, *Pseudoplectania*, and *Phytophthora*; more preferably the strain is selected from the group consisting of *Acremonium thermophilum*, *Chaetomium thermophilum*, *Scytalidium thermophilum*, *Thermoascus aurantiacus*, *Thielavia australiensis*, *Verticillium tenerum*, *Neotermes castaneus*, *Melanocarpus albomyces*, *Poitrasia circinans*, *Coprinus cinereus*, *Trichothecium roseum*, *Humicola nigrescens*, *Cladorrhinum foecundissimum*, *Diplodia gossypina*, *Myceliophthora thermophila*, *Rhizomucor pusillus*, *Meripilus giganteus*, *Exidia glandulosa*, *Xylaria hypoxylon*, *Trichophaea saccata*, *Chaetomidium pingtungium*, *Myceliophthora thermophila*, *Myceliophthora hinnulea*, *Sporotrichum pruinosum*, *Thielavia cf. microspora*, *Pseudoplectania nigrella*, and *Phytophthora infestans*.

The present invention also relates to methods for producing a polypeptide of the present invention comprising (a) cultivating a host cell under conditions conducive for production of the polypeptide; and (b) recovering the polypeptide.

The present invention also relates to methods for in-situ production of a polypeptide of the present invention comprising (a) cultivating a host cell under conditions conducive for production of the polypeptide; and (b) contacting the polypeptide with a desired substrate, such as a cellulosic substrate, without prior recovery of the polypeptide. The term "in-situ production" is intended to mean that the polypeptide is produced directly in the locus in which it is intended to be used, such as in a fermentation process for production of ethanol.

In the production methods of the present invention, the cells are cultivated in a nutrient medium suitable for production of the polypeptide using methods known in the art. For example, the cell may be cultivated by shake flask cultivation, small-scale or large-scale fermentation (including continuous, batch, fed-batch, or solid state fermentations) in laboratory or industrial fermentors performed in a suitable medium and under conditions allowing the polypeptide to be expressed and/or isolated. The cultivation takes place in a suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures known in the art. Suitable media are available from commercial suppliers or may be prepared according to published compositions (e.g., in catalogues of the American Type Culture Collection). If the polypeptide is secreted into the nutrient medium, the polypeptide can be recovered directly from the medium. If the polypeptide is not secreted, it can be recovered from cell lysates.

The polypeptides may be detected using methods known in the art that are specific for the polypeptides. These detection methods may include use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme substrate. For example, an enzyme assay may be used to determine the activity of the polypeptide as described herein.

The resulting polypeptide may be recovered by methods known in the art. For example,

the polypeptide may be recovered from the nutrient medium by conventional procedures including, but not limited to, centrifugation, filtration, extraction, spray-drying, evaporation, or precipitation.

The polypeptides of the present invention may be purified by a variety of procedures known in the art including, but not limited to, chromatography (e.g., ion exchange, affinity, hydrophobic, chromatofocusing, and size exclusion), electrophoretic procedures (e.g., preparative isoelectric focusing), differential solubility (e.g., ammonium sulfate precipitation), SDS-PAGE, or extraction (see, e.g., *Protein Purification*, J.-C. Janson and Lars Ryden, editors, VCH Publishers, New York, 1989).

Plants

The present invention also relates to a transgenic plant, plant part, or plant cell which has been transformed with a nucleotide sequence encoding a polypeptide having cellobiohydrolase I activity of the present invention so as to express and produce the polypeptide in recoverable quantities. The polypeptide may be recovered from the plant or plant part. Alternatively, the plant or plant part containing the recombinant polypeptide may be used as such for improving the quality of a food or feed, e.g., improving nutritional value, palatability, and rheological properties, or to destroy an antinutritive factor.

The transgenic plant can be dicotyledonous (a dicot) or monocotyledonous (a monocot). Examples of monocot plants are grasses, such as meadow grass (blue grass, *Poa*), forage grass such as *Festuca*, *Lolium*, temperate grass, such as *Agrostis*, and cereals, e.g., wheat, oats, rye, barley, rice, sorghum, millets, and maize (corn).

Examples of dicot plants are tobacco, lupins, potato, sugar beet, legumes, such as pea, bean and soybean, and cruciferous plants (family *Brassicaceae*), such as cauliflower, rape, canola, and the closely related model organism *Arabidopsis thaliana*.

Examples of plant parts are stem, callus, leaves, root, fruits, seeds, and tubers. Also specific plant tissues, such as chloroplast, apoplast, mitochondria, vacuole, peroxisomes, and cytoplasm are considered to be a plant part. Furthermore, any plant cell, whatever the tissue origin, is considered to be a plant part.

Also included within the scope of the present invention are the progeny (clonal or seed) of such plants, plant parts and plant cells.

The transgenic plant or plant cell expressing a polypeptide of the present invention may be constructed in accordance with methods known in the art. Briefly, the plant or plant cell is constructed by incorporating one or more expression constructs encoding a polypeptide of the present invention into the plant host genome and propagating the resulting modified plant or plant cell into a transgenic plant or plant cell.

Conveniently, the expression construct is a nucleic acid construct which comprises a

nucleotide sequence encoding a polypeptide of the present invention operably linked with appropriate regulatory sequences required for expression of the nucleotide sequence in the plant or plant part of choice. Furthermore, the expression construct may comprise a selectable marker useful for identifying host cells into which the expression construct has been integrated and DNA sequences necessary for introduction of the construct into the plant in question (the latter depends on the DNA introduction method to be used).

The choice of regulatory sequences, such as promoter and terminator sequences and optionally signal or transit sequences is determined, for example, on the basis of when, where, and how the polypeptide is desired to be expressed. For instance, the expression of the gene encoding a polypeptide of the present invention may be constitutive or inducible, or may be developmental, stage or tissue specific, and the gene product may be targeted to a specific tissue or plant part such as seeds or leaves. Regulatory sequences are, for example, described by Tague *et al.*, 1988, *Plant Physiology* 86: 506.

For constitutive expression, the 35S-CaMV promoter may be used (Franck *et al.*, 1980, *Cell* 21: 285-294). Organ-specific promoters may be, for example, a promoter from storage sink tissues such as seeds, potato tubers, and fruits (Edwards & Coruzzi, 1990, *Ann. Rev. Genet.* 24: 275-303), or from metabolic sink tissues such as meristems (Ito *et al.*, 1994, *Plant Mol. Biol.* 24: 863-878), a seed specific promoter such as the glutelin, prolamin, globulin, or albumin promoter from rice (Wu *et al.*, 1998, *Plant and Cell Physiology* 39: 885-889), a *Vicia faba* promoter from the legumin B4 and the unknown seed protein gene from *Vicia faba* (Conrad *et al.*, 1998, *Journal of Plant Physiology* 152: 708-711), a promoter from a seed oil body protein (Chen *et al.*, 1998, *Plant and Cell Physiology* 39: 935-941), the storage protein napA promoter from *Brassica napus*, or any other seed specific promoter known in the art, e.g., as described in WO 91/14772. Furthermore, the promoter may be a leaf specific promoter such as the *rbcs* promoter from rice or tomato (Kyoizuka *et al.*, 1993, *Plant Physiology* 102: 991-1000, the chlorella virus adenine methyltransferase gene promoter (Mitra and Higgins, 1994, *Plant Molecular Biology* 26: 85-93), or the *aldP* gene promoter from rice (Kagaya *et al.*, 1995, *Molecular and General Genetics* 248: 668-674), or a wound inducible promoter such as the potato pin2 promoter (Xu *et al.*, 1993, *Plant Molecular Biology* 22: 573-588).

A promoter enhancer element may also be used to achieve higher expression of the enzyme in the plant. For instance, the promoter enhancer element may be an intron which is placed between the promoter and the nucleotide sequence encoding a polypeptide of the present invention. For instance, Xu *et al.*, 1993, *supra* disclose the use of the first intron of the rice actin 1 gene to enhance expression.

The selectable marker gene and any other parts of the expression construct may be chosen from those available in the art.

The nucleic acid construct is incorporated into the plant genome according to conventional techniques known in the art, including *Agrobacterium*-mediated transformation, virus-mediated transformation, microinjection, particle bombardment, biolistic transformation, and electroporation (Gasser *et al.*, 1990, *Science* 244: 1293; Potrykus, 1990, *Bio/Technology* 8: 535; Shimamoto *et al.*, 1989, *Nature* 338: 274).

Presently, *Agrobacterium tumefaciens*-mediated gene transfer is the method of choice for generating transgenic dicots (for a review, see Hooykas and Schilperoort, 1992, *Plant Molecular Biology* 19: 15-38). However it can also be used for transforming monocots, although other transformation methods are generally preferred for these plants. Presently, the method of choice for generating transgenic monocots is particle bombardment (microscopic gold or tungsten particles coated with the transforming DNA) of embryonic calli or developing embryos (Christou, 1992, *Plant Journal* 2: 275-281; Shimamoto, 1994, *Current Opinion Biotechnology* 5: 158-162; Vasil *et al.*, 1992, *Bio/Technology* 10: 667-674). An alternative method for transformation of monocots is based on protoplast transformation as described by Omirulleh *et al.*, 1993, *Plant Molecular Biology* 21: 415-428.

Following transformation, the transformants having incorporated therein the expression construct are selected and regenerated into whole plants according to methods well-known in the art.

The present invention also relates to methods for producing a polypeptide of the present invention comprising (a) cultivating a transgenic plant or a plant cell comprising a nucleotide sequence encoding a polypeptide having cellobiohydrolase I activity of the present invention under conditions conducive for production of the polypeptide; and (b) recovering the polypeptide.

The present invention also relates to methods for in-situ production of a polypeptide of the present invention comprising (a) cultivating a transgenic plant or a plant cell comprising a nucleotide sequence encoding a polypeptide having cellobiohydrolase I activity of the present invention under conditions conducive for production of the polypeptide; and (b) contacting the polypeptide with a desired substrate, such as a cellulosic substrate, without prior recovery of the polypeptide.

Compositions

In a still further aspect, the present invention relates to compositions comprising a polypeptide of the present invention.

The composition may comprise a polypeptide of the invention as the major enzymatic component, *e.g.*, a mono-component composition. Alternatively, the composition may comprise multiple enzymatic activities, such as an aminopeptidase, amylase, carbohydrase, carboxypeptidase, catalase, cellulase, chitinase, cutinase, cyclodextrin glycosyltransferase,

deoxyribonuclease, esterase, alpha-galactosidase, beta-galactosidase, glucoamylase, alpha-glucosidase, beta-glucosidase, haloperoxidase, invertase, laccase, lipase, mannosidase, oxidase, pectinolytic enzyme, peptidoglutaminase, peroxidase, phytase, polyphenoloxidase, proteolytic enzyme, ribonuclease, transglutaminase, or xylanase.

5 The compositions may be prepared in accordance with methods known in the art and may be in the form of a liquid or a dry composition. For instance, the polypeptide composition may be in the form of a granulate or a microgranulate. The polypeptide to be included in the composition may be stabilized in accordance with methods known in the art.

10 Examples are given below of preferred uses of the polypeptide compositions of the invention. The dosage of the polypeptide composition of the invention and other conditions under which the composition is used may be determined on the basis of methods known in the art.

Detergent Compositions

15 The polypeptide of the invention may be added to and thus become a component of a detergent composition.

20 The detergent composition of the invention may for example be formulated as a hand or machine laundry detergent composition including a laundry additive composition suitable for pre-treatment of stained fabrics and a rinse added fabric softener composition, or be formulated as a detergent composition for use in general household hard surface cleaning operations, or be formulated for hand or machine dishwashing operations.

25 In a specific aspect, the invention provides a detergent additive comprising the polypeptide of the invention. The detergent additive as well as the detergent composition may comprise one or more other enzymes such as a protease, a lipase, a cutinase, an amylase, a carbohydrase, a cellulase, a pectinase, a mannanase, an arabinase, a galactanase, a xylanase, an oxidase, e.g., a laccase, and/or a peroxidase.

 In general the properties of the chosen enzyme(s) should be compatible with the selected detergent, (i.e. pH-optimum, compatibility with other enzymatic and non-enzymatic ingredients, etc.), and the enzyme(s) should be present in effective amounts.

30 Proteases: Suitable proteases include those of animal, vegetable or microbial origin. Microbial origin is preferred. Chemically modified or protein engineered mutants are included. The protease may be a serine protease or a metallo protease, preferably an alkaline microbial protease or a trypsin-like protease. Examples of alkaline proteases are subtilisins, especially those derived from *Bacillus*, e.g., subtilisin Novo, subtilisin Carlsberg, subtilisin 309, subtilisin 147 and subtilisin 168 (described in WO 89/06279). Examples of trypsin-like proteases are trypsin (e.g. of porcine or bovine origin) and the *Fusarium* protease described in WO 89/06270 and WO 94/25583.

Examples of useful proteases are the variants described in WO 92/19729, WO 98/20115, WO 98/20116, and WO 98/34946, especially the variants with substitutions in one or more of the following positions: 27, 36, 57, 76, 87, 97, 101, 104, 120, 123, 167, 170, 194, 206, 218, 222, 224, 235 and 274.

5 Lipases: Suitable lipases include those of bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Examples of useful lipases include lipases from *Humicola* (synonym *Thermomyces*), e.g. from *H. lanuginosa* (*T. lanuginosus*) as described in EP 258 068 and EP 305 216 or from *H. insolens* as described in WO 96/13580, a *Pseudomonas* lipase, e.g. from *P. alcaligenes* or *P. pseudoalcaligenes* (EP 218 272), *P.*
10 *cepacia* (EP 331 376), *P. stutzeri* (GB 1,372,034), *P. fluorescens*, *Pseudomonas* sp. strain SD 705 (WO 95/06720 and WO 96/27002), *P. wisconsinensis* (WO 96/12012), a *Bacillus* lipase, e.g. from *B. subtilis* (Dartois et al. (1993), Biochemica et Biophysica Acta, 1131, 253-360), *B. stearothermophilus* (JP 64/744992) or *B. pumilus* (WO 91/16422).

Other examples are lipase variants such as those described in WO 92/05249, WO
15 94/01541, EP 407 225, EP 260 105, WO 95/35381, WO 96/00292, WO 95/30744, WO 94/25578, WO 95/14783, WO 95/22615, WO 97/04079 and WO 97/07202.

Amylases: Suitable amylases (alpha and/or beta) include those of bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Amylases include, for example, alpha-amylases obtained from *Bacillus*, e.g. a special strain of *B. licheniformis*,
20 described in more detail in GB 1,296,839.

Examples of useful amylases are the variants described in WO 94/02597, WO 94/18314, WO 96/23873, and WO 97/43424, especially the variants with substitutions in one or more of the following positions: 15, 23, 105, 106, 124, 128, 133, 154, 156, 181, 188, 190, 197, 202, 208, 209, 243, 264, 304, 305, 391, 408, and 444.

25 Cellulases: Suitable cellulases include those of bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Suitable cellulases include cellulases from the genera *Bacillus*, *Pseudomonas*, *Humicola*, *Fusarium*, *Thielavia*, *Acremonium*, e.g. the fungal cellulases produced from *Humicola insolens*, *Myceliophthora thermophila* and *Fusarium oxysporum* disclosed in US 4,435,307, US 5,648,263, US 5,691,178, US 5,776,757 and WO
30 89/09259.

Especially suitable cellulases are the alkaline or neutral cellulases having colour care benefits. Examples of such cellulases are cellulases described in EP 0 495 257, EP 0 531 372, WO 96/11262, WO 96/29397, WO 98/08940. Other examples are cellulase variants such as those described in WO 94/07998, EP 0 531 315, US 5,457,046, US 5,686,593, US
35 5,763,254, WO 95/24471, WO 98/12307 and PCT/DK98/00299.

Peroxidases/Oxidases: Suitable peroxidases/oxidases include those of plant, bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Examples of

useful peroxidases include peroxidases from *Coprinus*, e.g. from *C. cinereus*, and variants thereof as those described in WO 93/24618, WO 95/10602, and WO 98/15257.

The detergent enzyme(s) may be included in a detergent composition by adding separate additives containing one or more enzymes, or by adding a combined additive comprising all of these enzymes. A detergent additive of the invention, i.e. a separate additive or a combined additive, can be formulated e.g. as a granulate, a liquid, a slurry, etc. Preferred detergent additive formulations are granulates, in particular non-dusting granulates, liquids, in particular stabilized liquids, or slurries.

Non-dusting granulates may be produced, e.g., as disclosed in US 4,106,991 and 4,661,452 and may optionally be coated by methods known in the art. Examples of waxy coating materials are poly(ethylene oxide) products (polyethyleneglycol, PEG) with mean molar weights of 1000 to 20000; ethoxylated nonylphenols having from 16 to 50 ethylene oxide units; ethoxylated fatty alcohols in which the alcohol contains from 12 to 20 carbon atoms and in which there are 15 to 80 ethylene oxide units; fatty alcohols; fatty acids; and mono- and di- and triglycerides of fatty acids. Examples of film-forming coating materials suitable for application by fluid bed techniques are given in GB 1483591. Liquid enzyme preparations may, for instance, be stabilized by adding a polyol such as propylene glycol, a sugar or sugar alcohol, lactic acid or boric acid according to established methods. Protected enzymes may be prepared according to the method disclosed in EP 238,216.

The detergent composition of the invention may be in any convenient form, e.g., a bar, a tablet, a powder, a granule, a paste or a liquid. A liquid detergent may be aqueous, typically containing up to 70 % water and 0-30 % organic solvent, or non-aqueous.

The detergent composition comprises one or more surfactants, which may be non-ionic including semi-polar and/or anionic and/or cationic and/or zwitterionic. The surfactants are typically present at a level of from 0.1% to 60% by weight.

When included therein the detergent will usually contain from about 1% to about 40% of an anionic surfactant such as linear alkylbenzenesulfonate, alpha-olefinsulfonate, alkyl sulfate (fatty alcohol sulfate), alcohol ethoxysulfate, secondary alkanesulfonate, alpha-sulfo fatty acid methyl ester, alkyl- or alkenylsuccinic acid or soap.

When included therein the detergent will usually contain from about 0.2% to about 40% of a non-ionic surfactant such as alcohol ethoxylate, nonylphenol ethoxylate, alkylpolyglycoside, alkyldimethylamineoxide, ethoxylated fatty acid monoethanolamide, fatty acid monoethanolamide, polyhydroxy alkyl fatty acid amide, or N-acyl N-alkyl derivatives of glucosamine ("glucamides").

The detergent may contain 0-65 % of a detergent builder or complexing agent such as zeolite, diphosphate, triphosphate, phosphonate, carbonate, citrate, nitrilotriacetic acid, ethylenediaminetetraacetic acid, diethylenetriaminepentaacetic acid, alkyl- or alkenylsuccinic

acid, soluble silicates or layered silicates (e.g. SKS-6 from Hoechst).

The detergent may comprise one or more polymers. Examples are carboxymethylcellulose, poly(vinylpyrrolidone), poly (ethylene glycol), poly(vinyl alcohol), poly(vinylpyridine-N-oxide), poly(vinylimidazole), polycarboxylates such as polyacrylates, maleic/acrylic acid copolymers and lauryl methacrylate/acrylic acid copolymers.

The detergent may contain a bleaching system which may comprise a H₂O₂ source such as perborate or percarbonate which may be combined with a peracid-forming bleach activator such as tetraacetythylenediamine or nonanoyloxybenzenesulfonate. Alternatively, the bleaching system may comprise peroxyacids of e.g. the amide, imide, or sulfone type.

The enzyme(s) of the detergent composition of the invention may be stabilized using conventional stabilizing agents, e.g., a polyol such as propylene glycol or glycerol, a sugar or sugar alcohol, lactic acid, boric acid, or a boric acid derivative, e.g., an aromatic borate ester, or a phenyl boronic acid derivative such as 4-formylphenyl boronic acid, and the composition may be formulated as described in e.g. WO 92/19709 and WO 92/19708.

The detergent may also contain other conventional detergent ingredients such as e.g. fabric conditioners including clays, foam boosters, suds suppressors, anti-corrosion agents, soil-suspending agents, anti-soil redeposition agents, dyes, bactericides, optical brighteners, hydrotropes, tarnish inhibitors, or perfumes.

It is at present contemplated that in the detergent compositions any enzyme, in particular the polypeptide of the invention, may be added in an amount corresponding to 0.01-100 mg of enzyme protein per liter of wash liquor, preferably 0.05-5 mg of enzyme protein per liter of wash liquor, in particular 0.1-1 mg of enzyme protein per liter of wash liquor.

The polypeptide of the invention may additionally be incorporated in the detergent formulations disclosed in WO 97/07202 which is hereby incorporated as reference.

DNA recombination (shuffling)

The nucleotide sequences of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:67 may be used in a DNA recombination (or shuffling) process. The new polynucleotide sequences obtained in such a process may encode new polypeptides having cellobiase activity with improved properties, such as improved stability (storage stability, thermostability), improved specific activity, improved pH-optimum, and/or improved tolerance towards specific compounds.

Shuffling between two or more homologous input polynucleotides (starting-point polynucleotides) involves fragmenting the polynucleotides and recombining the fragments, to obtain output polynucleotides (i.e. polynucleotides that have been subjected to a shuffling cycle) wherein a number of nucleotide fragments are exchanged in comparison to the input polynucleotides.

DNA recombination or shuffling may be a (partially) random process in which a library of chimeric genes is generated from two or more starting genes. A number of known formats can be used to carry out this shuffling or recombination process.

The process may involve random fragmentation of parental DNA followed by reassembly by PCR to new full-length genes, e.g. as presented in US5605793, US5811238, US5830721, US6117679. In-vitro recombination of genes may be carried out, e.g. as described in US6159687, WO98/41623, US6159688, US5965408, US6153510. The recombination process may take place in vivo in a living cell, e.g. as described in WO 97/07205 and WO 98/28416.

The parental DNA may be fragmented by DNA'se I treatment or by restriction endonuclease digests as described by Kikuchi et al (2000a, Gene 236:159-167). Shuffling of two parents may be done by shuffling single stranded parental DNA of the two parents as described in Kikuchi et al (2000b, Gene 243:133-137).

A particular method of shuffling is to follow the methods described in Crameri et al, 1998, Nature, 391: 288-291 and Ness et al. Nature Biotechnology 17: 893-896. Another format would be the methods described in US 6159687: Examples 1 and 2.

Production of Ethanol from Biomass

The present invention also relates to methods for producing ethanol from biomass, such as cellulosic materials, comprising contacting the biomass with the polypeptides of the invention. Ethanol may subsequently be recovered. The polypeptides of the invention may be produced "in-situ", i.e., as part of, or directly in an ethanol production process, by cultivating a host cell or a strain, which in its wild-type form is capable of producing the polypeptides, under conditions conducive for production of the polypeptides.

Ethanol can be produced by enzymatic degradation of biomass and conversion of the released polysaccharides to ethanol. This kind of ethanol is often referred to as bioethanol or biofuel. It can be used as a fuel additive or extender in blends of from less than 1% and up to 100% (a fuel substitute). In some countries, such as Brazil, ethanol is substituting gasoline to a very large extent.

The predominant polysaccharide in the primary cell wall of biomass is cellulose, the second most abundant is hemi-cellulose, and the third is pectin. The secondary cell wall, produced after the cell has stopped growing, also contains polysaccharides and is strengthened through polymeric lignin covalently cross-linked to hemicellulose. Cellulose is a

homopolymer of anhydrocellobiose and thus a linear beta-(1-4)-D-glucan, while hemicelluloses include a variety of compounds, such as xylans, xyloglucans, arabinoxylans, and mannans in complex branched structures with a spectrum of substituents. Although generally polymorphous, cellulose is found in plant tissue primarily as an insoluble crystalline matrix of parallel glucan chains. Hemicelluloses usually hydrogen bond to cellulose, as well as to other hemicelluloses, which helps stabilize the cell wall matrix.

Three major classes of cellulase enzymes are used to breakdown biomass:

- The "endo-1,4-beta-glucanases" or 1,4-beta-D-glucan-4-glucanohydrolases (EC 3.2.1.4), which act randomly on soluble and insoluble 1,4-beta-glucan substrates.
- The "exo-1,4-beta-D-glucanases" including both the 1,4-beta-D-glucan glucohydrolases (EC 3.2.1.74), which liberate D-glucose from 1,4-beta-D-glucans and hydrolyze D-cellobiose slowly, and 1,4-beta-D-glucan cellobiohydrolase (EC 3.2.1.91), also referred to as cellobiohydrolase I, which liberates D-cellobiose from 1,4-beta-glucans.
- The "beta-D-glucosidases" or beta-D-glucoside glucohydrolases (EC 3.2.1.21), which act to release D-glucose units from cellobiose and soluble cellodextrins, as well as an array of glycosides.

These three classes of enzymes work together synergistically in a complex interplay that results in efficient decrystallization and hydrolysis of native cellulose from biomass to yield the reducing sugars which are converted to ethanol by fermentation.

The present invention is further described by the following examples which should not be construed as limiting the scope of the invention.

EXAMPLES

Chemicals used as buffers and substrates were commercial products of at least reagent grade.

EXAMPLE 1

Cloning of a partial and a full-length cellobiohydrolase I (CBH1) DNA sequence

A cDNA library of *Diplodia gossypina* was PCR screened for presence of the CBH1 gene. For this purpose sets of primers were constructed, based on sequence alignment and identification of conserved regions among CBH1 proteins. The PCR band from a gel electrophoresis was used to obtain a partial sequence of the CBH1 gene from *Diplodia gossypina*. Homology search confirmed that the partial sequence was a partial sequence of the CBH1 gene (EC 3.2.1.91).

The full-length CBH1 gene of *Diplodia gossypina* is obtained by accessing the patent deposit CBS 247.96, make a DNA or cDNA preparation, use the partial sequence as basis for construction of specific primers, and use standard PCR cloning techniques to step by step getting the entire gene.

Several other approaches can be taken:

- PCR screening of the cDNA library or the cDNAs that were used for the construction of the library, could be performed. To do so, Gene Specific Primers (GSP) and vector/adaptor primers are constructed from the partial cDNA sequence of the CBH1 gene and from vector/adaptor sequence respectively; both sets of primers designed to go outward into the missing 5' and 3' regions of the CBH1 cDNA. The longest PCR products obtained using combinations of GSP and vector/adaptor primer represent the full-length 5' and 3' end regions of the CBH1 cDNA from *Diplodia gossypina*. Homology search and comparison with the partial cDNA sequence confirm that the 5' and 3' PCR products belong to the same CBH1 cDNA from *Diplodia gossypina*. The full-length cDNA can then be obtained by PCR using a set of primers constructed from both the 5' and 3' ends.
- Alternatively, the cDNA library could be screened for the full-length cDNA using standard hybridization techniques and the partial cDNA sequence as a probe. The clones giving a positive hybridization signal with the probe are then purified and sequenced to determine the longest cDNA sequence. Homology search and comparison confirms that the full-length cDNA correspond to the partial CBH1 cDNA sequence that was originally used as a probe.

The two approaches described above rely on the presence of the full-length CBH1 cDNA in the cDNA library or in the cDNAs used for its construction. Alternatively, the 5' and 3' RACE (Rapid Amplification of cDNA Ends) techniques or derived techniques could be used to identify the missing 5' and 3' regions. For this purpose, preferably mRNAs from *Diplodia gossypina* are isolated and utilized to synthesize first strand cDNAs using oligo(dT)-containing Adapter Primer or a 5'- Gene Specific Primer (GSP).

The full-length cDNA of the CBH1 gene from *Diplodia gossypina* can also be obtained by using genomic DNA from *Diplodia gossypina*. The CBH1 gene can be identified by PCR techniques such as the one describe above or by standard genomic library screening using hybridization techniques and the partial CBH1 cDNA as a probe. Homology search and

comparison with the partial CBH1 cDNA confirms that the genomic sequence correspond to the CBH1 gene from *Diplodia gossypina*. Identification of consensus sequences such as initiation site of transcription, start and stop codons or polyA sites could be used to defined the region comprising the full-length cDNA. Primers constructed from both the 5' and 3' ends of this region could then be used to amplify the full-length cDNA from mRNA or cDNA library from *Diplodia gossypina* (see above).

By expression of the full-length gene in a suitable expression host construct the CBH1 enzyme is harvested as an intra cellular or extra cellular enzyme from the culture broth.

The methods described above apply to the cloning of cellobiohydrolase I DNA sequences from all organisms and not only *Diplodia gossypina*.

EXAMPLE 2

Cellobiohydrolase I (CBH I) Activity

A cellobiohydrolase I is characterized by the ability to hydrolyze highly crystalline cellulose very efficiently compared to other cellulases. Cellobiohydrolase I may have a higher catalytic activity using PASC (phosphoric acid swollen cellulose) as substrate than using CMC as substrate. For the purposes of the present invention, any of the following assays can be used to identify a cellobiohydrolase I:

Activity on Azo-Avicel

Azo-Avicel (Megazyme, Bray Business Park, Bray, Wicklow, Ireland) was used according to the manufacturers instructions.

Activity on PNP-beta-cellobiose

Substrate solution: 5 mM PNP beta-D-Cellobiose (p-Nitrophenyl β -D-Cellobioside Sigma N-5759) in 0.1 M Na-acetate buffer, pH 5.0;

Stop reagent: 0.1 M Na-carbonate, pH 11.5.

50 μ L CBH I solution was mixed with 1 mL substrate solution and incubated 20 minutes at 40°C. The reaction was stopped by addition of 5 mL stop reagent. Absorbance was measured at 404 nm.

Activity on PASC and CMC

The substrate is degraded with cellobiohydrolase I (CBH I) to form reducing sugars. A

Microdochium nivale carbohydrate oxidase (rMnO) or another equivalent oxidase acts on the reducing sugars to form H_2O_2 in the presence of O_2 . The formed H_2O_2 activates in the presence of excess peroxidase the oxidative condensation of 4-aminoantipyrine (AA) and N-ethyl-N-sulfopropyl-m-toluidine (TOPS) to form a purple product which can be quantified by its absorbance at 550 nm.

When all components except CBH I are in surplus, the rate of increase in absorbance is proportional to the CBH I activity. The reaction is a one-kinetic-step reaction and may be carried out automatically in a Cobas Fara centrifugal analyzer (Hoffmann La Roche) or another equivalent spectrophotometer which can measure steady state kinetics.

Buffer: 50 mM Na-acetate buffer (pH 5.0);

Reagents: rMnO oxidase, purified *Microdochium nivale* carbohydrate oxidase, 2 mg/L (final concentration);

Peroxidase, SIGMA P-8125 (96 U/mg), 25 mg/L (final concentration);

4-aminoantipyrine, SIGMA A-4382, 200 mg/L (final concentration);

TOPS, SIGMA E-8506, 600 mg/L (final concentration);

PASC or CMC (see below), 5 g/L (final concentration).

All reagents were added to the buffer in the concentrations indicated above and this reagent solution was mixed thoroughly.

50 μ L cellobiohydrolase I sample (in a suitable dilution) was mixed with 300 μ L reagent solution and incubated 20 minutes at 40°C. Purple color formation was detected and measured as absorbance at 550 nm.

The AA/TOPS-condensate absorption coefficient is 0.01935 $A_{550}/(\mu M \text{ cm})$. The rate is calculated as μ moles reducing sugar produced per minute from OD_{550}/minute and the absorption coefficient.

PASC:

Materials: 5 g Avicel® (Art. 2331 Merck);

150 mL 85% Ortho-phosphoric-acid (Art. 573 Merck);

800 mL Acetone (Art. 14 Merck);

Approx. 2 liter deionized water (Milli-Q);

1 L glass beaker;

1 L glass filter funnel;

2 L suction flask;

Ultra Turrax Homogenizer.

Acetone and ortho-phosphoric-acid is cooled on ice. Avicel® is moistened with water, and then the 150 mL icecold 85% Ortho-phosphoric-acid is added. The mixture is placed on an

icebath with weak stirring for one hour.

Add 500 mL ice-cold acetone with stirring, and transfer the mixture to a glass filter funnel and wash with 3 x 100 mL ice-cold acetone, suck as dry as possible in each wash. Wash with 2 x 500 mL water (or until there is no odor of acetone), suck as dry as possible in each wash.

- 5 Re-suspend the solids in water to a total volume of 500 mL, and blend to homogeneity using an Ultra Turrax Homogenizer. Store wet in refrigerator and equilibrate with buffer by centrifugation and re-suspension before use.

CMC:

- 10 Bacterial cellulose microfibrils in an impure form was obtained from the Japanese foodstuff "nata de coco" (Fujico Company, Japan). The cellulose in 350 g of this product was purified by suspension of the product in about 4 L of tap water. This water was replaced by fresh water twice a day for 4 days.

- 15 Then 1% (w/v) NaOH was used instead of water and the product was re-suspended in the alkali solution twice a day for 4 days. Neutralisation was done by rinsing the purified cellulose with distilled water until the pH at the surface of the product was neutral (pH 7).

- 20 The cellulose was microfibrillated and a suspension of individual bacterial cellulose microfibrils was obtained by homogenisation of the purified cellulose microfibrils in a Waring blender for 30 min. The cellulose microfibrils were further purified by dialysing this suspension through a pore membrane against distilled water and the isolated and purified cellulose microfibrils were stored in a water suspension at 4°C.

Deposit of Biological Material

25

China General Microbiological Culture Collection Center (CGMCC)

The following biological material has been deposited under the terms of the Budapest Treaty with the China General Microbiological Culture Collection Center (CGMCC), Institute of Microbiology, Chinese Academy of Sciences, Haidian, Beijing 100080, China:

30

Accession Number:	CGMCC No. 0584
Applicants reference:	ND000575
Date of Deposit:	2001-05-29
Description:	<i>Acremonium thermophilum</i> CBH I gene on plasmid
35 Classification:	<i>Ascomycota; Sordariomycetes; Hypocrales; Hypocreaceae</i>
Origin:	China, 1999
Related sequence(s):	SEQ ID NO:1 and SEQ ID NO:2 (DNA sequence encoding a

cellobiohydrolase I from *Acremonium thermophilum* and the corresponding protein sequence)

- Accession Number: **CGMCC No. 0581**
- 5 Applicants reference: ND000548
- Date of Deposit: 2001-05-29
- Description: *Chaetomium thermophilum* CBH I gene on plasmid
- Classification: *Ascomycota; Sordariomycetes; Sordariales; Chaetomiaceae*
- Origin: China, 1999
- 10 Related sequence(s): SEQ ID NO:3 and SEQ ID NO:4 (DNA sequence encoding a cellobiohydrolase I from *Chaetomium thermophilum* and the corresponding protein sequence)
-
- Accession Number: **CGMCC No. 0585**
- 15 Applicants reference: ND001223
- Date of Deposit: 2001-05-29
- Description: *Scytalidium* sp. CBH I gene on plasmid
- Classification: *Ascomycota; Mitosporic*
- Origin: China, 1999
- 20 Related sequence(s): SEQ ID NO:5 and SEQ ID NO:6 (DNA sequence encoding a cellobiohydrolase I from *Scytalidium* sp. and the corresponding protein sequence)
-
- Accession Number: **CGMCC No. 0582**
- 25 Applicants reference: ND000549
- Date of Deposit: 2001-05-29
- Description: *Thermoascus aurantiacus* CBH I gene on plasmid
- Classification: *Eurotiomycetes; Eurotiales; Trichocomaceae*
- Origin: China
- 30 Related sequence(s): SEQ ID NO:7 and SEQ ID NO:8 (DNA sequence encoding a cellobiohydrolase I from *Thermoascus aurantiacus* and the corresponding protein sequence)
-
- Accession Number: **CGMCC No. 0583**
- 35 Applicants reference: ND001182
- Date of Deposit: 2001-05-29
- Description: *Thielavia australiensis* CBH I gene on plasmid

Classification: *Ascomycota; Sordariomycetes; Sordariales; Chaetomiaceae*
 Origin: China, 1998
 Related sequence(s): SEQ ID NO:9 and SEQ ID NO:10 (DNA sequence encoding a cellobiohydrolase I from *Thielavia australiensis* and the corresponding protein sequence)

5

Accession Number: **CGMCC No. 0580**
 Applicants reference: ND000562
 Date of Deposit: 2001-05-29
 Description: *Melanocarpus albomyces* CBH I gene on plasmid
 Classification: *Ascomycota; Sordariomycetes; Sordariales*
 Origin: China, 1999
 Related sequence(s): SEQ ID NO:15 and SEQ ID NO:16 (DNA sequence encoding a cellobiohydrolase I from *Melanocarpus albomyces* and the corresponding protein sequence)

10

15

Accession Number: **CGMCC No. 0748**
 Applicants reference: ND001181
 Date of Deposit: 2002-06-07
 Description: *Acremonium* sp. CBH I gene on plasmid
 Classification: mitosporic *Ascomycetes*
 Origin: China, 2000
 Related sequence(s): SEQ ID NO:53 and SEQ ID NO:54

20

25

Accession Number: **CGMCC No. 0749**
 Applicants reference: ND000577
 Date of Deposit: 2002-06-07
 Description: *Chaetomidium pingtungium* CBH I gene on plasmid
 Classification: *Chaetomiaceae, Sordariales, Ascomycota*
 Origin: China, 2000
 Related sequence(s): SEQ ID NO:55 and SEQ ID NO:56

30

Accession Number: **CGMCC No. 0747**
 Applicants reference: ND001175
 Date of Deposit: 2002-06-07
 Description: *Sporotrichum pruinosum* CBH I gene on plasmid
 Classification: *Meruliaceae, Stereales, Basidiomycota*

35

Origin: China, 2000
 Related sequence(s): SEQ ID NO:57 and SEQ ID NO:58

Accession Number: **CGMCC No. 0750**

5 Applicants reference: ND000571

Date of Deposit: 2002-06-07

Description: *Scytalidium thermophilum* CBH I gene on plasmid

Classification: *Ascomycota; Mitosporic*

Origin: China, 2000

10 Related sequence(s): SEQ ID NO:59 and SEQ ID NO:60

Centraalbureau Voor Schimmelcultures (CBS)

15 The following biological material has been deposited under the terms of the Budapest Treaty with the Centraalbureau Voor Schimmelcultures (CBS), Uppsalalaan 8, 3584 CT Utrecht, The Netherlands (alternatively P.O.Box 85167, 3508 AD Utrecht, The Netherlands):

Accession Number: **CBS 109513**

Applicants reference: ND000538

20 Date of Deposit: 2001-06-01

Description: *Verticillium tenerum*

Classification: *Ascomycota, Hypocreales, Pyrenomyces* (mitosporic)

Origin: -

25 Related sequence(s): SEQ ID NO:11 and SEQ ID NO:12 (DNA sequence encoding a cellobiohydrolase I from *Verticillium tenerum* and the corresponding protein sequence)

Accession Number: **CBS 819.73**

Applicants reference: ND000533

30 Date of Deposit: Publicly available (not deposited by applicant)

Description: *Humicola nigrescens*

Classification: *Sordariaceae, Sordariales, Sordariomycetes; Ascomycota*

Origin: -

35 Related sequence(s): SEQ ID NO:18 (partial DNA sequence encoding a cellobiohydrolase I from *Humicola nigrescens*)

Accession Number: **CBS 427.97**

- Applicants reference: ND000530
 Date of Deposit: 1997-01-23
 Description: *Cladorrhinum foecundissimum*
 Classification: *Sordariaceae, Sordariales, Sordariomycetes; Ascomycota*
 5 Origin: Jamaica
 Related sequence(s): SEQ ID NO:19 (partial DNA sequence encoding a cellobiohydrolase I from *Cladorrhinum foecundissimum*)
- Accession Number: **CBS 247.96**
 10 Applicants reference: ND000534 and ND001231
 Date of Deposit: 1996-03-12
 Description: *Diplodia gossypina*
 Classification: *Dothideaceae, Dothideales, Dothidemyces; Ascomycota*
 Origin: Indonesia, 1992
 15 Related sequence(s): SEQ ID NO:20 (partial DNA sequence encoding a cellobiohydrolase I from *Diplodia gossypina*), SEQ ID NO:37 (full DNA sequence encoding a cellobiohydrolase I from *Diplodia gossypina*) and SEQ ID NO:38 (full cellobiohydrolase I protein sequence from *Diplodia gossypina*)
- 20
 Accession Number: **CBS 117.65**
 Applicants reference: ND000536
 Date of Deposit: Publicly available
 Description: *Myceliophthora thermophila*
 25 Classification: *Sordariaceae, Sordariales, Sordariomycetes; Ascomycota*
 Origin: -
 Related sequence(s): SEQ ID NO:21 (partial DNA sequence encoding a cellobiohydrolase I from *Myceliophthora thermophila*)
- 30
 Accession Number: **CBS 109471**
 Applicants reference: ND000537
 Date of Deposit: 2001-05-29
 Description: *Rhizomucor pusillus*
 Classification: *Mucoraceae, Mucorales, Zygomycota*
 35 Origin: Denmark
 Related sequence(s): SEQ ID NO:22 (partial DNA sequence encoding a cellobiohydrolase I from *Rhizomucor pusillus*)

- Accession Number: **CBS 521.95**
Applicants reference: ND000542
Date of Deposit: 1995-07-04
5 Description: *Meripilus giganteus*
Classification: *Rigidiporaceae, Hymenomycetales, Basidiomycota*
Origin: Denmark, 1993
Related sequence(s): SEQ ID NO:23 (partial DNA sequence encoding a cellobiohydrolase I from *Meripilus giganteus*)
- 10
Accession Number: **CBS 277.96**
Applicants reference: ND000543, ND001346 and ND001243
Date of Deposit: 1996-03-12
Description: *Exidia glandulosa*
15 Classification: *Exidiaceae, Auriculariales, Hymenomycetes, Basidiomycota*
Origin: Denmark, 1993
Related sequence(s): SEQ ID NO:24 (partial DNA sequence encoding a cellobiohydrolase I from *Exidia glandulosa*), SEQ ID NO:45 (full DNA sequence encoding a cellobiohydrolase I with CBD from *Exidia glandulosa*),
20 SEQ ID NO:46 (full cellobiohydrolase I protein sequence with CBD from *Exidia glandulosa*), SEQ ID NO:47 (full DNA sequence encoding a cellobiohydrolase I from *Exidia glandulosa*) and SEQ ID NO:48 (full cellobiohydrolase I protein sequence from *Exidia glandulosa*)
- 25
Accession Number: **CBS 284.96**
Applicants reference: ND000544 and ND001235
Date of Deposit: 1996-03-12
Description: *Xylaria hypoxylon*
30 Classification: *Sordariaceae, Sordariales, Sordariomycetes, Ascomycota*
Origin: Denmark, 1993
Related sequence(s): SEQ ID NO:25 (partial DNA sequence encoding a cellobiohydrolase I from *Xylaria hypoxylon*), SEQ ID NO:43 (full DNA sequence encoding a cellobiohydrolase I from *Xylaria hypoxylon*) and SEQ ID
35 NO:44 (full cellobiohydrolase I protein sequence from *Xylaria hypoxylon*)

Accession Number: **CBS 804.70**

Applicants reference: ND001227

Date of Deposit: Publicly available

Description: *Trichophaea saccata*

5 Classification: *Ascomycota; Pezizomycetes; Pezizales; Pyronemataceae*

Related sequence(s): SEQ ID NO:36 (partial DNA sequence encoding a cellobiohydrolase I from *Trichophaea saccata*)

10 Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ)

The following biological material has been deposited under the terms of the Budapest Treaty with the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ), Mascheroder Weg 1b, 38124 Braunschweig, Germany:

15 Accession Number: **DSM 14348**

Applicants reference: ND000551

Date of Deposit: 2001-06-13

Description: *Neotermes castaneus*, termite CBH I gene on plasmid

Classification: -

20 Origin: Cultures of termite larvae bought from BAM, Germany, 1999

Related sequence(s): SEQ ID NO:13 and SEQ ID NO:14 (DNA sequence encoding a cellobiohydrolase I from gut cells or microbes from the gut of *Neotermes castaneus* and the corresponding protein sequence)

25 Accession Number: **DSM 15066**

Applicants reference: ND001349

Date of Deposit: 2002-06-21

Description: *Poitrasia circinans* CBH I gene on plasmid

Classification: *Choanephoraceae, Zygomycota, Mucorales*

30 Origin: -

Related sequence(s): SEQ ID NO:49 (DNA sequence encoding a cellobiohydrolase I from *Poitrasia circinans*) and SEQ ID NO:50 (cellobiohydrolase I protein sequence from *Poitrasia circinans*)

35 Accession Number: **DSM 15065**

Applicants reference: ND001339

Date of Deposit: 2002-06-21

Description: *Coprinus cinereus* CBH I gene on plasmid
Classification: *Basidiomycota, Hymenomycetes; Agaricales, Agaricaceae*
Origin: Denmark
Related sequence(s): SEQ ID NO:51 (DNA sequence encoding a cellobiohydrolase I from
5 *Coprinus cinereus*) and SEQ ID NO:52 (cellobiohydrolase I protein
sequence from *Coprinus cinereus*)

Accession Number: **DSM 15064**

Applicants reference: ND001264

10 Date of Deposit: 2002-06-21

Description: *Trichophaea saccata* CBH I gene on plasmid

Classification: *Ascomycota; Pezizomycetes; Pezizales; Pyronemataceae*

Origin: -

15 Related sequence(s): SEQ ID NO:39 (DNA sequence encoding a cellobiohydrolase I from
Trichophaea saccata) and SEQ ID NO:40 (cellobiohydrolase I
protein sequence from *Trichophaea saccata*)

Accession Number: **DSM 15067**

Applicants reference: ND001232

20 Date of Deposit: 2002-06-21

Description: *Myceliophthora thermophila* CBH I gene on plasmid

Classification: *Sordariaceae, Sordariales, Sordariomycetes; Ascomycota*

Origin: -

25 Related sequence(s): SEQ ID NO:41 (DNA sequence encoding a cellobiohydrolase I from
Myceliophthora thermophila) and SEQ ID NO:42 (cellobiohydrolase I
protein sequence from *Myceliophthora thermophila*)

Institute for Fermentation, Osaka (IFO)

30 The following biological material has been deposited under the terms of the Budapest
Treaty with the Institute for Fermentation, Osaka (IFO), 17-85, Juso-honmachi 2-chome,
Yodogawa-ku, Osaka 532-8686, Japan:

Accession Number: **IFO 5372**

35 Applicants reference: ND000531

Date of Deposit: Publicly available (not deposited by applicant)

Description: *Trichothecium roseum*

Classification: mitosporic *Ascomycetes*
Origin: -
Related sequence(s): SEQ ID NO:17 (partial DNA sequence encoding a cellobiohydrolase I from *Trichothecium roseum*)

5

The deposit of CBS 427.97, CBS 247.96, CBS 521.95, CBS 284.96, CBS 274.96 were made by Novo Nordisk A/S and were later assigned to Novozymes A/S.

0-1	Form - PCT/RO/134 (EASY) Indications Relating to Deposited Microorganism(s) or Other Biological Material (PCT Rule 13bis)	
0-1-1	Prepared using	PCT-EASY Version 2.92 (updated 01.06.2002)
0-2	International Application No.	
0-3	Applicant's or agent's file reference	10129.204-WO
1	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
1-1	page	63-64
1-2	line	31-2
1-3	Identification of Deposit	
1-3-1	Name of depositary institution	China General Microbiological Culture Collection Center
1-3-2	Address of depositary institution	China Committee for Culture Collection of Microorganisms, P.O. Box 2714, Beijing 100080, China
1-3-3	Date of deposit	29 May 2001 (29.05.2001)
1-3-4	Accession Number	CGMCC 0584
1-4	Additional Indications	NONE
1-5	Designated States for Which Indications are Made	all designated States
1-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
2	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
2-1	page	64
2-2	line	4-12
2-3	Identification of Deposit	
2-3-1	Name of depositary institution	China General Microbiological Culture Collection Center
2-3-2	Address of depositary institution	China Committee for Culture Collection of Microorganisms, P.O. Box 2714, Beijing 100080, China
2-3-3	Date of deposit	29 May 2001 (29.05.2001)
2-3-4	Accession Number	CGMCC 0581
2-4	Additional Indications	NONE
2-5	Designated States for Which Indications are Made	all designated States
2-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE

3	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
3-1	page	64
3-2	line	14-22
3-3	Identification of Deposit	
3-3-1	Name of depositary institution	China General Microbiological Culture Collection Center
3-3-2	Address of depositary institution	China Committee for Culture Collection of Microorganisms, P.O. Box 2714, Beijing 100080, China
3-3-3	Date of deposit	29 May 2001 (29.05.2001)
3-3-4	Accession Number	CGMCC 0585
3-4	Additional Indications	NONE
3-5	Designated States for Which Indications are Made	all designated States
3-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
4	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
4-1	page	64
4-2	line	24-32
4-3	Identification of Deposit	
4-3-1	Name of depositary institution	China General Microbiological Culture Collection Center
4-3-2	Address of depositary institution	China Committee for Culture Collection of Microorganisms, P.O. Box 2714, Beijing 100080, China
4-3-3	Date of deposit	29 May 2001 (29.05.2001)
4-3-4	Accession Number	CGMCC 0582
4-4	Additional Indications	NONE
4-5	Designated States for Which Indications are Made	all designated States
4-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
5	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
5-1	page	64-65
5-2	line	34-5

5-3	Identification of Deposit	
5-3-1	Name of depositary institution	China General Microbiological Culture Collection Center
5-3-2	Address of depositary institution	China Committee for Culture Collection of Microorganisms, P.O. Box 2714, Beijing 100080, China
5-3-3	Date of deposit	29 May 2001 (29.05.2001)
5-3-4	Accession Number	CGMCC 0583
5-4	Additional Indications	NONE
5-5	Designated States for Which Indications are Made	all designated States
5-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
6	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
6-1	page	65
6-2	line	7-15
6-3	Identification of Deposit	
6-3-1	Name of depositary institution	China General Microbiological Culture Collection Center
6-3-2	Address of depositary institution	China Committee for Culture Collection of Microorganisms, P.O. Box 2714, Beijing 100080, China
6-3-3	Date of deposit	29 May 2001 (29.05.2001)
6-3-4	Accession Number	CGMCC 0580
6-4	Additional Indications	NONE
6-5	Designated States for Which Indications are Made	all designated States
6-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
7	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
7-1	page	65
7-2	line	17-23
7-3	Identification of Deposit	
7-3-1	Name of depositary institution	Centre Général Chinois de Cultures Microbiologiques
7-3-2	Address of depositary institution	Chine - Comité pour la collection de cultures de micro-organismes, P.O. Box 2714, Beijing 100080
7-3-3	Date of deposit	07 June 2002 (07.06.2002)
7-3-4	Accession Number	CGCCM 0748
7-4	Additional Indications	NONE

7-5	Designated States for Which Indications are Made	all designated States
7-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
8	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
8-1	page	65
8-2	line	25-31
8-3	Identification of Deposit	
8-3-1	Name of depositary institution	Centre Général Chinois de Cultures Microbiologiques
8-3-2	Address of depositary institution	Chine - Comité pour la collection de cultures de micro-organismes, P.O. Box 2714, Beijing 100080
8-3-3	Date of deposit	07 June 2002 (07.06.2002)
8-3-4	Accession Number	CGCCM 0749
8-4	Additional Indications	NONE
8-5	Designated States for Which Indications are Made	all designated States
8-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
9	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
9-1	page	65-66
9-2	line	33-2
9-3	Identification of Deposit	
9-3-1	Name of depositary institution	Centre Général Chinois de Cultures Microbiologiques
9-3-2	Address of depositary institution	Chine - Comité pour la collection de cultures de micro-organismes, P.O. Box 2714, Beijing 100080
9-3-3	Date of deposit	07 June 2002 (07.06.2002)
9-3-4	Accession Number	CGCCM 0747
9-4	Additional Indications	NONE
9-5	Designated States for Which Indications are Made	all designated States
9-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
10	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
10-1	page	66
10-2	line	4-10

10-3	Identification of Deposit	
10-3-1	Name of depositary institution	Centre Général Chinois de Cultures Microbiologiques
10-3-2	Address of depositary institution	Chine - Comité pour la collection de cultures de micro-organismes, P.O. Box 2714, Beijing 100080
10-3-3	Date of deposit	07 June 2002 (07.06.2002)
10-3-4	Accession Number	CGCCM 0750
10-4	Additional Indications	NONE
10-5	Designated States for Which Indications are Made	all designated States
10-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
11	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
11-1	page	66
11-2	line	18-26
11-3	Identification of Deposit	
11-3-1	Name of depositary institution	Centraalbureau voor Schimmelcultures
11-3-2	Address of depositary institution	Uppsalalaan 8, NL-3584 CT Utrecht, The Netherlands / P.O. Box 85167, NL-3508 AD Utrecht, The Netherlands
11-3-3	Date of deposit	01 June 2001 (01.06.2001)
11-3-4	Accession Number	CBS 109513
11-4	Additional Indications	NONE
11-5	Designated States for Which Indications are Made	all designated States
11-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
12	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
12-1	page	66-67
12-2	line	37-7
12-3	Identification of Deposit	
12-3-1	Name of depositary institution	Centraalbureau voor Schimmelcultures
12-3-2	Address of depositary institution	Uppsalalaan 8, NL-3584 CT Utrecht, The Netherlands / P.O. Box 85167, NL-3508 AD Utrecht, The Netherlands
12-3-3	Date of deposit	23 January 1997 (23.01.1997)
12-3-4	Accession Number	CBS 427.97
12-4	Additional Indications	NONE
12-5	Designated States for Which Indications are Made	all designated States

12-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
13	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
13-1	page	67
13-2	line	9-19
13-3	Identification of Deposit	
13-3-1	Name of depositary institution	Centraalbureau voor Schimmelcultures
13-3-2	Address of depositary institution	Uppsalalaan 8, NL-3584 CT Utrecht, The Netherlands / P.O. Box 85167, NL-3508 AD Utrecht, The Netherlands
13-3-3	Date of deposit	12 March 1996 (12.03.1996)
13-3-4	Accession Number	CBS 247.96
13-4	Additional Indications	NONE
13-5	Designated States for Which Indications are Made	all designated States
13-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
14	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
14-1	page	67
14-2	line	30-37
14-3	Identification of Deposit	
14-3-1	Name of depositary institution	Centraalbureau voor Schimmelcultures
14-3-2	Address of depositary institution	Uppsalalaan 8, NL-3584 CT Utrecht, The Netherlands / P.O. Box 85167, NL-3508 AD Utrecht, The Netherlands
14-3-3	Date of deposit	29 May 2001 (29.05.2001)
14-3-4	Accession Number	CBS 109471
14-4	Additional Indications	NONE
14-5	Designated States for Which Indications are Made	all designated States
14-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
15	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
15-1	page	68
15-2	line	2-9

15-3	Identification of Deposit	
15-3-1	Name of depositary institution	Centraalbureau voor Schimmelcultures
15-3-2	Address of depositary institution	Uppsalalaan 8, NL-3584 CT Utrecht, The Netherlands / P.O. Box 85167, NL-3508 AD Utrecht, The Netherlands
15-3-3	Date of deposit	04 July 1995 (04.07.1995)
15-3-4	Accession Number	CBS 521.95
15-4	Additional Indications	NONE
15-5	Designated States for Which Indications are Made	all designated States
15-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
16	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
16-1	page	68
16-2	line	26-36
16-3	Identification of Deposit	
16-3-1	Name of depositary institution	Centraalbureau voor Schimmelcultures
16-3-2	Address of depositary institution	Uppsalalaan 8, NL-3584 CT Utrecht, The Netherlands / P.O. Box 85167, NL-3508 AD Utrecht, The Netherlands
16-3-3	Date of deposit	12 March 1996 (12.03.1996)
16-3-4	Accession Number	CBS 284.96
16-4	Additional Indications	NONE
16-5	Designated States for Which Indications are Made	all designated States
16-6	Separate Furnishing of Indications	NONE
	These indications will be submitted to the International Bureau later	
17	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
17-1	page	68
17-2	line	11-24
17-3	Identification of Deposit	
17-3-1	Name of depositary institution	Centraalbureau voor Schimmelcultures
17-3-2	Address of depositary institution	Uppsalalaan 8, NL-3584 CT Utrecht, The Netherlands / P.O. Box 85167, NL-3508 AD Utrecht, The Netherlands
17-3-3	Date of deposit	12 March 1996 (12.03.1996)
17-3-4	Accession Number	CBS 277.96
17-4	Additional Indications	NONE
17-5	Designated States for Which Indications are Made	all designated States

17-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
18	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
18-1	page	69
18-2	line	15-23
18-3	Identification of Deposit	
18-3-1	Name of depositary institution	DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH
18-3-2	Address of depositary institution	Mascheroder Weg 1b, D-38124 Braunschweig, Germany
18-3-3	Date of deposit	13 June 2001 (13.06.2001)
18-3-4	Accession Number	DSMZ 14348
18-4	Additional Indications	NONE
18-5	Designated States for Which Indications are Made	all designated States
18-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
19	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
19-1	page	69
19-2	line	25-33
19-3	Identification of Deposit	
19-3-1	Name of depositary institution	DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH
19-3-2	Address of depositary institution	Mascheroder Weg 1b, D-38124 Braunschweig, Germany
19-3-3	Date of deposit	21 June 2002 (21.06.2002)
19-3-4	Accession Number	DSMZ 15066
19-4	Additional Indications	NONE
19-5	Designated States for Which Indications are Made	all designated States
19-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
20	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
20-1	page	69-70
20-2	line	35-6

20-3	Identification of Deposit	
20-3-1	Name of depositary institution	DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH
20-3-2	Address of depositary institution	Mascheroder Weg 1b, D-38124 Braunschweig, Germany
20-3-3	Date of deposit	21 June 2002 (21.06.2002)
20-3-4	Accession Number	DSMZ 15065
20-4	Additional Indications	NONE
20-5	Designated States for Which Indications are Made	all designated States
20-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
21	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
21-1	page	70
21-2	line	8-16
21-3	Identification of Deposit	
21-3-1	Name of depositary institution	DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH
21-3-2	Address of depositary institution	Mascheroder Weg 1b, D-38124 Braunschweig, Germany
21-3-3	Date of deposit	21 June 2002 (21.06.2002)
21-3-4	Accession Number	DSMZ 15064
21-4	Additional Indications	NONE
21-5	Designated States for Which Indications are Made	all designated States
21-6	Separate Furnishing of Indications These indications will be submitted to the International Bureau later	NONE
22	The indications made below relate to the deposited microorganism(s) or other biological material referred to in the description on:	
22-1	page	70
22-2	line	18-26
22-3	Identification of Deposit	
22-3-1	Name of depositary institution	DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH
22-3-2	Address of depositary institution	Mascheroder Weg 1b, D-38124 Braunschweig, Germany
22-3-3	Date of deposit	21 June 2002 (21.06.2002)
22-3-4	Accession Number	DSMZ 15067
22-4	Additional Indications	NONE
22-5	Designated States for Which Indications are Made	all designated States

Claims

1. A polypeptide having cellobiohydrolase I activity, selected from the group consisting of:

- 5 (a) a polypeptide comprising an amino acid sequence selected from the group consisting of:
an amino acid sequence which has at least 80% identity with amino acids 1 to 526 of
SEQ ID NO:2,
an amino acid sequence which has at least 80% identity with amino acids 1 to 529 of
SEQ ID NO:4,
10 an amino acid sequence which has at least 80% identity with amino acids 1 to 451 of
SEQ ID NO:6,
an amino acid sequence which has at least 80% identity with amino acids 1 to 457 of
SEQ ID NO:8,
an amino acid sequence which has at least 80% identity with amino acids 1 to 538 of
15 SEQ ID NO:10,
an amino acid sequence which has at least 70% identity with amino acids 1 to 415 of
SEQ ID NO:12,
an amino acid sequence which has at least 70% identity with amino acids 1 to 447 of
SEQ ID NO:14,
20 an amino acid sequence which has at least 80% identity with amino acids 1 to 452 of
SEQ ID NO:16,
an amino acid sequence which has at least 80% identity with amino acids 1 to 454 of
SEQ ID NO:38,
an amino acid sequence which has at least 80% identity with amino acids 1 to 458 of
25 SEQ ID NO:40,
an amino acid sequence which has at least 80% identity with amino acids 1 to 450 of
SEQ ID NO:42,
an amino acid sequence which has at least 80% identity with amino acids 1 to 446 of
SEQ ID NO:44,
30 an amino acid sequence which has at least 80% identity with amino acids 1 to 527 of
SEQ ID NO:46,
an amino acid sequence which has at least 80% identity with amino acids 1 to 455 of
SEQ ID NO:48,
an amino acid sequence which has at least 80% identity with amino acids 1 to 464 of
35 SEQ ID NO:50,
an amino acid sequence which has at least 80% identity with amino acids 1 to 460 of
SEQ ID NO:52,

an amino acid sequence which has at least 80% identity with amino acids 1 to 450 of SEQ ID NO:54,

an amino acid sequence which has at least 80% identity with amino acids 1 to 532 of SEQ ID NO:56,

5 an amino acid sequence which has at least 80% identity with amino acids 1 to 460 of SEQ ID NO:58,

an amino acid sequence which has at least 80% identity with amino acids 1 to 525 of SEQ ID NO:60, and

10 an amino acid sequence which has at least 80% identity with amino acids 1 to 456 of SEQ ID NO:66;

(b) a polypeptide comprising an amino acid sequence selected from the group consisting of:

15 an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Acremonium thermophilum*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Chaetomium thermophilum*,

20 an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Scytalidium* sp.,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Scytalidium thermophilum*,

25 an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Thermoascus aurantiacus*,

30 an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Thielavia australiensis*,

an amino acid sequence which has at least 70% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Verticillium tenerum*,

35 an amino acid sequence which has at least 70% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Neotermes castaneus*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by

the cellobiohydrolase I encoding part of the nucleotide sequence present in *Melanocarpus albomyces*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Acremonium* sp.,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Chaetomidium pingtungium*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Sporotrichum pruinosum*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Diplodia gossypina*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Trichophaea saccata*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Myceliophthora thermophila*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Exidia glandulosa*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Xylaria hypoxylon*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Poitrasia circinans*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Coprinus cinereus*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Pseudoplectania nigrella*,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Trichothecium roseum* IFO 5372,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Humicola nigrescens* CBS 819.73,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Cladorrhinum foecundissimum* CBS 427.97,

5 an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Diplodia gossypina* CBS 247.96,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Myceliophthora thermophila* CBS 117.65,

10 an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Rhizomucor pusillus* CBS 109471,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Meripilus giganteus* CBS 521.95,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Exidia glandulosa* CBS 2377.96,

15 an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Xylaria hypoxylon* CBS 284.96,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Trichophaea saccata* CBS 804.70,

20 an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Chaetomium* sp.,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Myceliophthora hinnulea*,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Thielavia cf. microspora*,

25 an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Aspergillus* sp.,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Scopulariopsis* sp.,

30 an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Fusarium* sp.,

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Verticillium* sp., and

an amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in *Phytophthora infestans*;

35

- (c) a polypeptide comprising an amino acid sequence selected from the group consisting of:
an amino acid sequence which has at least 80% identity with the polypeptide encoded by

nucleotides 1 to 1578 of SEQ ID NO:1,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1587 of SEQ ID NO:3,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
5 nucleotides 1 to 1353 of SEQ ID NO:5,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1371 of SEQ ID NO:7,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1614 of SEQ ID NO:9,
10 an amino acid sequence which has at least 70% identity with the polypeptide encoded by
nucleotides 1 to 1245 of SEQ ID NO:11,
an amino acid sequence which has at least 70% identity with the polypeptide encoded by
nucleotides 1 to 1341 of SEQ ID NO:13,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
15 nucleotides 1 to 1356 of SEQ ID NO:15,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1365 of SEQ ID NO:37,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1377 of SEQ ID NO:39,
20 an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1353 of SEQ ID NO:41,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1341 of SEQ ID NO:43,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
25 nucleotides 1 to 1584 of SEQ ID NO:45,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1368 of SEQ ID NO:47,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1395 of SEQ ID NO:49,
30 an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1383 of SEQ ID NO:51,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1353 of SEQ ID NO:53,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
35 nucleotides 1 to 1599 of SEQ ID NO:55,
an amino acid sequence which has at least 80% identity with the polypeptide encoded by
nucleotides 1 to 1383 of SEQ ID NO:57,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by nucleotides 1 to 1578 of SEQ ID NO:59, and
 an amino acid sequence which has at least 80% identity with the polypeptide encoded by nucleotides 1 to 1371 of SEQ ID NO:65;

5

(d) a polypeptide which is encoded by a nucleotide sequence which hybridizes under high stringency conditions with a polynucleotide probe selected from the group consisting of:

(i) the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 1 to 1578 of SEQ ID NO:1,
 nucleotides 1 to 1587 of SEQ ID NO:3,
 nucleotides 1 to 1353 of SEQ ID NO:5,
 nucleotides 1 to 1371 of SEQ ID NO:7,
 nucleotides 1 to 1614 of SEQ ID NO:9,
 nucleotides 1 to 1245 of SEQ ID NO:11,
 nucleotides 1 to 1341 of SEQ ID NO:13,
 nucleotides 1 to 1356 of SEQ ID NO:15,
 nucleotides 1 to 1365 of SEQ ID NO:37,
 nucleotides 1 to 1377 of SEQ ID NO:39,
 nucleotides 1 to 1353 of SEQ ID NO:41,
 nucleotides 1 to 1341 of SEQ ID NO:43,
 nucleotides 1 to 1584 of SEQ ID NO:45,
 nucleotides 1 to 1368 of SEQ ID NO:47,
 nucleotides 1 to 1395 of SEQ ID NO:49,
 nucleotides 1 to 1383 of SEQ ID NO:51,
 nucleotides 1 to 1353 of SEQ ID NO:53,
 nucleotides 1 to 1599 of SEQ ID NO:55,
 nucleotides 1 to 1383 of SEQ ID NO:57,
 nucleotides 1 to 1578 of SEQ ID NO:59, and
 nucleotides 1 to 1371 of SEQ ID NO:65;

(ii) the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 1 to 500 of SEQ ID NO:1,
 nucleotides 1 to 500 of SEQ ID NO:3,
 nucleotides 1 to 500 of SEQ ID NO:5,
 nucleotides 1 to 500 of SEQ ID NO:7,
 nucleotides 1 to 500 of SEQ ID NO:9,
 nucleotides 1 to 500 of SEQ ID NO:11,
 nucleotides 1 to 500 of SEQ ID NO:13,

5 nucleotides 1 to 500 of SEQ ID NO:15,
nucleotides 1 to 500 of SEQ ID NO:37,
nucleotides 1 to 500 of SEQ ID NO:39,
nucleotides 1 to 500 of SEQ ID NO:41,
nucleotides 1 to 500 of SEQ ID NO:43,
nucleotides 1 to 500 of SEQ ID NO:45,
nucleotides 1 to 500 of SEQ ID NO:47,
nucleotides 1 to 500 of SEQ ID NO:49,
nucleotides 1 to 500 of SEQ ID NO:51,
10 nucleotides 1 to 500 of SEQ ID NO:53,
nucleotides 1 to 500 of SEQ ID NO:55,
nucleotides 1 to 500 of SEQ ID NO:57,
nucleotides 1 to 500 of SEQ ID NO:59,
nucleotides 1 to 500 of SEQ ID NO:65,
15 nucleotides 1 to 221 of SEQ ID NO:17,
nucleotides 1 to 239 of SEQ ID NO:18,
nucleotides 1 to 199 of SEQ ID NO:19,
nucleotides 1 to 191 of SEQ ID NO:20,
nucleotides 1 to 232 of SEQ ID NO:21,
20 nucleotides 1 to 467 of SEQ ID NO:22,
nucleotides 1 to 534 of SEQ ID NO:23,
nucleotides 1 to 563 of SEQ ID NO:24,
nucleotides 1 to 218 of SEQ ID NO:25,
nucleotides 1 to 492 of SEQ ID NO:26,
25 nucleotides 1 to 481 of SEQ ID NO:27,
nucleotides 1 to 463 of SEQ ID NO:28,
nucleotides 1 to 513 of SEQ ID NO:29,
nucleotides 1 to 579 of SEQ ID NO:30,
nucleotides 1 to 514 of SEQ ID NO:31,
30 nucleotides 1 to 477 of SEQ ID NO:32,
nucleotides 1 to 500 of SEQ ID NO:33,
nucleotides 1 to 470 of SEQ ID NO:34,
nucleotides 1 to 491 of SEQ ID NO:35,
nucleotides 1 to 221 of SEQ ID NO:36,
35 nucleotides 1 to 519 of SEQ ID NO:61,
nucleotides 1 to 497 of SEQ ID NO:62,
nucleotides 1 to 498 of SEQ ID NO:63,

nucleotides 1 to 525 of SEQ ID NO:64, and
nucleotides 1 to 951 of SEQ ID NO:67; and

(iii) the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 1 to 200 of SEQ ID NO:1,
nucleotides 1 to 200 of SEQ ID NO:3,
nucleotides 1 to 200 of SEQ ID NO:5,
nucleotides 1 to 200 of SEQ ID NO:7,
nucleotides 1 to 200 of SEQ ID NO:9,
nucleotides 1 to 200 of SEQ ID NO:11,
nucleotides 1 to 200 of SEQ ID NO:13,
nucleotides 1 to 200 of SEQ ID NO:15,
nucleotides 1 to 200 of SEQ ID NO:37,
nucleotides 1 to 200 of SEQ ID NO:39,
nucleotides 1 to 200 of SEQ ID NO:41,
nucleotides 1 to 200 of SEQ ID NO:43,
nucleotides 1 to 200 of SEQ ID NO:45,
nucleotides 1 to 200 of SEQ ID NO:47,
nucleotides 1 to 200 of SEQ ID NO:49,
nucleotides 1 to 200 of SEQ ID NO:51,
nucleotides 1 to 200 of SEQ ID NO:53,
nucleotides 1 to 200 of SEQ ID NO:55,
nucleotides 1 to 200 of SEQ ID NO:57,
nucleotides 1 to 200 of SEQ ID NO:59, and
nucleotides 1 to 200 of SEQ ID NO:65; and

(e) a fragment of (a), (b) or (c) that has cellobiohydrolase I activity.

2. The polypeptide according to claim 1, comprising an amino acid sequence selected from the group consisting of:

an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity, with amino acids 1 to 526 of SEQ ID NO:2;

an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity, with amino acids 1 to 529 of SEQ ID NO:4,

an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity, with amino acids 1 to 451 of SEQ ID NO:6,

an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity, with amino acids 1 to 457 of SEQ ID NO:8,

an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity, with amino acids 1 to 538 of SEQ ID NO:10,

an amino acid sequence which has at least 75% identity, preferably at least 80% identity, more preferably at least 90% identity, with amino acids 1 to 415 of SEQ ID NO:12,

5 an amino acid sequence which has at least 75% identity, preferably at least 80% identity, more preferably at least 90% identity, with amino acids 1 to 447 of SEQ ID NO:14,

an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity, with amino acids 1 to 452 of SEQ ID NO:16,

10 an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity with amino acids 1 to 454 of SEQ ID NO:38,

an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity with amino acids 1 to 458 of SEQ ID NO:40,

an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity with amino acids 1 to 450 of SEQ ID NO:42,

15 an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity with amino acids 1 to 446 of SEQ ID NO:44,

an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity with amino acids 1 to 527 of SEQ ID NO:46,

20 an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity with amino acids 1 to 455 of SEQ ID NO:48,

an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity with amino acids 1 to 464 of SEQ ID NO:50,

an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity with amino acids 1 to 460 of SEQ ID NO:52,

25 an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity with amino acids 1 to 450 of SEQ ID NO:54,

an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity with amino acids 1 to 532 of SEQ ID NO:56,

30 an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity with amino acids 1 to 460 of SEQ ID NO:58,

an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity with amino acids 1 to 525 of SEQ ID NO:60, and

an amino acid sequence which has at least 85% identity, preferably at least 90% identity, more preferably at least 95% identity with amino acids 1 to 456 of SEQ ID NO:66.

35

3. The polypeptide according to any of claims 1-2, which consists of an amino acid sequence selected from the group consisting of:

amino acids 1 to 526 of SEQ ID NO:2,
amino acids 1 to 529 of SEQ ID NO:4,
amino acids 1 to 451 of SEQ ID NO:6,
amino acids 1 to 457 of SEQ ID NO:8,
5 amino acids 1 to 538 of SEQ ID NO:10,
amino acids 1 to 415 of SEQ ID NO:12,
amino acids 1 to 447 of SEQ ID NO:14,
amino acids 1 to 452 of SEQ ID NO:16,
amino acids 1 to 454 of SEQ ID NO:38,
10 amino acids 1 to 458 of SEQ ID NO:40,
amino acids 1 to 450 of SEQ ID NO:42,
amino acids 1 to 446 of SEQ ID NO:44,
amino acids 1 to 527 of SEQ ID NO:46,
amino acids 1 to 455 of SEQ ID NO:48,
15 amino acids 1 to 464 of SEQ ID NO:50,
amino acids 1 to 460 of SEQ ID NO:52,
amino acids 1 to 450 of SEQ ID NO:54,
amino acids 1 to 532 of SEQ ID NO:56,
amino acids 1 to 460 of SEQ ID NO:58,
20 amino acids 1 to 525 of SEQ ID NO:60, and
amino acids 1 to 456 of SEQ ID NO:66.

4. The polypeptide according to any of claims 1-2, where the polypeptide is an artificial variant which comprises an amino acid sequence that has at least one substitution, deletion and/or
25 insertion of an amino acid as compared to an amino acid sequence selected from the group consisting of:

amino acids 1 to 526 of SEQ ID NO:2,
amino acids 1 to 529 of SEQ ID NO:4,
amino acids 1 to 451 of SEQ ID NO:6,
30 amino acids 1 to 457 of SEQ ID NO:8,
amino acids 1 to 538 of SEQ ID NO:10,
amino acids 1 to 415 of SEQ ID NO:12,
amino acids 1 to 447 of SEQ ID NO:14,
amino acids 1 to 452 of SEQ ID NO:16,
35 amino acids 1 to 454 of SEQ ID NO:38,
amino acids 1 to 458 of SEQ ID NO:40,
amino acids 1 to 450 of SEQ ID NO:42,

amino acids 1 to 446 of SEQ ID NO:44,
amino acids 1 to 527 of SEQ ID NO:46,
amino acids 1 to 455 of SEQ ID NO:48,
amino acids 1 to 464 of SEQ ID NO:50,
5 amino acids 1 to 460 of SEQ ID NO:52,
amino acids 1 to 450 of SEQ ID NO:54,
amino acids 1 to 532 of SEQ ID NO:56,
amino acids 1 to 460 of SEQ ID NO:58,
amino acids 1 to 525 of SEQ ID NO:60, and
10 amino acids 1 to 456 of SEQ ID NO:66.

5. The polypeptide according to claim 1, comprising an amino acid sequence selected from the group consisting of:
an amino acid sequence which has at least 80% identity, preferably at least 90% identity, with
15 the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CGMCC No. 0584,
an amino acid sequence which has at least 80% identity, preferably at least 90% identity, with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CGMCC No. 0581,
20 an amino acid sequence which has at least 80% identity, preferably at least 90% identity, with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CGMCC No. 0585,
an amino acid sequence which has at least 80% identity, preferably at least 90% identity, with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence
25 inserted into a plasmid present in the deposited microorganism CGMCC No. 0582,
an amino acid sequence which has at least 80% identity, preferably at least 90% identity, with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CGMCC No. 0583,
an amino acid sequence which has at least 80% identity, preferably at least 90% identity, with
30 the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CBS 109513,
an amino acid sequence which has at least 80% identity, preferably at least 90% identity, with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism DSM 14348,
35 an amino acid sequence which has at least 80% identity, preferably at least 90% identity, with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CGMCC No. 0580,

an amino acid sequence which has at least 80% identity, preferably at least 90% identity, with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CGMCC No. 0747,

an amino acid sequence which has at least 80% identity, preferably at least 90% identity, with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CGMCC No. 0748,

an amino acid sequence which has at least 80% identity, preferably at least 90% identity, with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CGMCC No. 0749,

an amino acid sequence which has at least 80% identity, preferably at least 90% identity, with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CGMCC No. 0750,

an amino acid sequence which has at least 80% identity, preferably at least 90% identity, with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism DSM 15064,

an amino acid sequence which has at least 80% identity, preferably at least 90% identity, with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism DSM 15065,

an amino acid sequence which has at least 80% identity, preferably at least 90% identity, with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism DSM 15066, and

an amino acid sequence which has at least 80% identity, preferably at least 90% identity, with the polypeptide encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism DSM 15067.

6. The polypeptide according to claim 5, which comprises the amino acid sequence encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in a deposited microorganism selected from the group consisting of:

CGMCC No. 0584,

CGMCC No. 0581,

CGMCC No. 0585,

CGMCC No. 0582,

CGMCC No. 0583,

CBS 109513,

DSM 14348,

CGMCC No. 0580,

CGMCC No. 0747,

CGMCC No. 0748,
CGMCC No. 0749,
CGMCC No. 0750,
DSM 15064,
5 DSM 15065,
DSM 15066, and
DSM 15067.

7. The polypeptide according to claims 5 or 6, which consists of the amino acid sequence
10 encoded by the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a
plasmid present in a deposited microorganism selected from the group consisting of:

CGMCC No. 0584,
CGMCC No. 0581,
CGMCC No. 0585,
15 CGMCC No. 0582,
CGMCC No. 0583,
CBS 109513,
DSM 14348,
CGMCC No. 0580,
20 CGMCC No. 0747,
CGMCC No. 0748,
CGMCC No. 0749,
CGMCC No. 0750,
DSM 15064,
25 DSM 15065,
DSM 15066, and
DSM 15067.

8. The polypeptide according to claims 5 or 6, where the polypeptide is an artificial variant
30 which comprises an amino acid sequence that has at least one substitution, deletion and/or
insertion of an amino acid as compared to the amino acid sequence encoded by the
cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in
a deposited microorganism selected from the group consisting of:

CGMCC No. 0584,
35 CGMCC No. 0581,
CGMCC No. 0585,
CGMCC No. 0582,

CGMCC No. 0583,
CBS 109513,
DSM 14348,
CGMCC No. 0580,
5 CGMCC No. 0747,
CGMCC No. 0748,
CGMCC No. 0749,
CGMCC No. 0750,
DSM 15064,
10 DSM 15065,
DSM 15066, and
DSM 15067.

9. A polynucleotide having a nucleotide sequence which encodes for the polypeptide defined
15 in any of claims 1-8.

10. A nucleic acid construct comprising the nucleotide sequence defined in claim 9 operably
linked to one or more control sequences that direct the production of the polypeptide in a
suitable host.

20 11. A recombinant expression vector comprising the nucleic acid construct defined in claim 10.

12. A recombinant host cell comprising the nucleic acid construct defined in claim 11.

25 13. A method for producing a polypeptide as defined in any of claims 1-8, the method
comprising:

- (a) cultivating a strain, which in its wild-type form is capable of producing the polypeptide, to
produce the polypeptide; and
- (b) recovering the polypeptide.

30 14. A method for producing a polypeptide as defined in any of claims 1-8, the method
comprising:

- (a) cultivating a recombinant host cell as defined in claim 12 under conditions conducive for
production of the polypeptide; and
- 35 (b) recovering the polypeptide.

15. A method for in-situ production of a polypeptide as defined in any of claims 1-8, the

method comprising:

- (a) cultivating a recombinant host cell as defined in claim 12 under conditions conducive for production of the polypeptide; and
- (b) contacting the polypeptide with a desired substrate without prior recovery of the polypeptide.

16. A polynucleotide comprising a nucleotide sequence selected from the group consisting of:
a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1578 of SEQ ID NO:1,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1587 of SEQ ID NO:3,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1353 of SEQ ID NO:5,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1371 of SEQ ID NO:7,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1614 of SEQ ID NO:9,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1245 of SEQ ID NO:11,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1341 of SEQ ID NO:13,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1356 of SEQ ID NO:15,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1365 of SEQ ID NO:37,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1377 of SEQ ID NO:39,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1353 of SEQ ID NO:41,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1341 of SEQ ID NO:43,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1584 of SEQ ID NO:45,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1368 of SEQ ID NO:47,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1395 of SEQ ID NO:49,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1383 of SEQ ID NO:51,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1353 of SEQ ID NO:53,

5 a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1599 of SEQ ID NO:55,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1383 of SEQ ID NO:57,

10 a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1578 of SEQ ID NO:59,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 1371 of SEQ ID NO:65,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID NO:1,

15 a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID NO:3,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID NO:5,

20 a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID NO:7,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID NO:9,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID NO:11,

25 a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID NO:13,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID NO:15,

30 a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID NO:37,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID NO:39,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID NO:41,

35 a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID NO:43,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID

- NO:45,
a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID
- NO:47,
a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID
- 5 NO:49,
a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID
- NO:51,
a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID
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10 a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID
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a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID
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a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID
- 15 NO:59,
a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID
- NO:65,
a nucleotide sequence which has at least 80% identity with nucleotides 1 to 221 of SEQ ID
- NO:17,
20 a nucleotide sequence which has at least 80% identity with nucleotides 1 to 239 of SEQ ID
- NO:18,
a nucleotide sequence which has at least 80% identity with nucleotides 1 to 199 of SEQ ID
- NO:19,
a nucleotide sequence which has at least 80% identity with nucleotides 1 to 191 of SEQ ID
- 25 NO:20,
a nucleotide sequence which has at least 80% identity with nucleotides 1 to 232 of SEQ ID
- NO:21,
a nucleotide sequence which has at least 80% identity with nucleotides 1 to 467 of SEQ ID
- NO:22,
30 a nucleotide sequence which has at least 80% identity with nucleotides 1 to 534 of SEQ ID
- NO:23,
a nucleotide sequence which has at least 80% identity with nucleotides 1 to 563 of SEQ ID
- NO:24,
a nucleotide sequence which has at least 80% identity with nucleotides 1 to 218 of SEQ ID
- 35 NO:25,
a nucleotide sequence which has at least 80% identity with nucleotides 1 to 492 of SEQ ID
- NO:26,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 481 of SEQ ID NO:27,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 463 of SEQ ID NO:28,

5 a nucleotide sequence which has at least 80% identity with nucleotides 1 to 513 of SEQ ID NO:29,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 579 of SEQ ID NO:30,

10 a nucleotide sequence which has at least 80% identity with nucleotides 1 to 514 of SEQ ID NO:31,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 477 of SEQ ID NO:32,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 500 of SEQ ID NO:33,

15 a nucleotide sequence which has at least 80% identity with nucleotides 1 to 470 of SEQ ID NO:34,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 491 of SEQ ID NO:35,

20 a nucleotide sequence which has at least 80% identity with nucleotides 1 to 221 of SEQ ID NO:36,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 519 of SEQ ID NO:61,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 497 of SEQ ID NO:62,

25 a nucleotide sequence which has at least 80% identity with nucleotides 1 to 498 of SEQ ID NO:63,

a nucleotide sequence which has at least 80% identity with nucleotides 1 to 525 of SEQ ID NO:64, and

30 a nucleotide sequence which has at least 80% identity with nucleotides 1 to 951 of SEQ ID NO:67.

17. A polynucleotide comprising a nucleotide sequence selected from the group consisting of:
a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding
part of the nucleotide sequence inserted into a plasmid present in the deposited
35 microorganism CGMCC No. 0584,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding
part of the nucleotide sequence inserted into a plasmid present in the deposited

microorganism CGMCC No. 0581,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CGMCC No. 0585,

5 a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CGMCC No. 0582,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited

10 microorganism CGMCC No. 0583,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CBS 109513,

15 a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism DSM 14348,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CGMCC No. 0580,

20 a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CGMCC No. 0747,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited

25 microorganism CGMCC No. 0748,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CGMCC No. 0749,

30 a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism CGMCC No. 0750,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism DSM 15064,

35 a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism DSM 15065,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism DSM 15066, and

5 a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence inserted into a plasmid present in the deposited microorganism DSM 15067.

18. A polynucleotide comprising a nucleotide sequence selected from the group consisting of:

10 a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Trichothecium roseum* IFO 5372,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Humicola nigrescens* CBS 819.73,

15 a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Cladorrhinum foecundissimum* CBS 427.97,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Diplodia gossypina* CBS 247.96,

20 a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Myceliophthora thermophila* CBS 117.65,

25 a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Rhizomucor pusillus* CBS 109471,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Meripilus giganteus* CBS 521.95,

30 a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Exidia glandulosa* CBS 2377.96,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Xylaria hypoxylon* CBS 284.96,

35 a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Trichophaea saccata* CBS 804.70,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Acremonium* sp.,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Chaetomium* sp.,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Chaetomidium pingtungium*,

5 a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Myceliophthora thermophila*,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Myceliophthora hinnulea*,

10 a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Sporotrichum pruinosum*,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Thielavia cf. microspora*, and

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Scytalidium* sp.,

15 a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Aspergillus* sp.,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Scopulariopsis* sp.,

20 a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Fusarium* sp.,

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Verticillium* sp., and

a nucleotide sequence which has at least 80% identity with the cellobiohydrolase I encoding part of the nucleotide sequence present in the microorganism *Phytophthora infestans*.

25

19. A polynucleotide having a nucleotide sequence which encodes a polypeptide having cellobiohydrolase I activity, and which hybridizes under high stringency conditions with a polynucleotide probe selected from the group consisting of

(i) the complementary strand of the nucleotides selected from the group consisting of:

30 nucleotides 1 to 1578 of SEQ ID NO:1,

nucleotides 1 to 1587 of SEQ ID NO:3,

nucleotides 1 to 1353 of SEQ ID NO:5,

nucleotides 1 to 1371 of SEQ ID NO:7,

nucleotides 1 to 1614 of SEQ ID NO:9,

35 nucleotides 1 to 1245 of SEQ ID NO:11,

nucleotides 1 to 1341 of SEQ ID NO:13,

nucleotides 1 to 1356 of SEQ ID NO:15,

- nucleotides 1 to 1365 of SEQ ID NO:37,
 nucleotides 1 to 1377 of SEQ ID NO:39,
 nucleotides 1 to 1353 of SEQ ID NO:41,
 nucleotides 1 to 1341 of SEQ ID NO:43,
 5 nucleotides 1 to 1584 of SEQ ID NO:45,
 nucleotides 1 to 1368 of SEQ ID NO:47,
 nucleotides 1 to 1395 of SEQ ID NO:49,
 nucleotides 1 to 1383 of SEQ ID NO:51,
 nucleotides 1 to 1353 of SEQ ID NO:53,
 10 nucleotides 1 to 1599 of SEQ ID NO:55,
 nucleotides 1 to 1383 of SEQ ID NO:57,
 nucleotides 1 to 1578 of SEQ ID NO:59, and
 nucleotides 1 to 1371 of SEQ ID NO:65;
- (ii) the complementary strand of the nucleotides selected from the group consisting of:
- 15 nucleotides 1 to 500 of SEQ ID NO:1,
 nucleotides 1 to 500 of SEQ ID NO:3,
 nucleotides 1 to 500 of SEQ ID NO:5,
 nucleotides 1 to 500 of SEQ ID NO:7,
 nucleotides 1 to 500 of SEQ ID NO:9,
 20 nucleotides 1 to 500 of SEQ ID NO:11,
 nucleotides 1 to 500 of SEQ ID NO:13,
 nucleotides 1 to 500 of SEQ ID NO:15,
 nucleotides 1 to 500 of SEQ ID NO:37,
 nucleotides 1 to 500 of SEQ ID NO:39,
 25 nucleotides 1 to 500 of SEQ ID NO:41,
 nucleotides 1 to 500 of SEQ ID NO:43,
 nucleotides 1 to 500 of SEQ ID NO:45,
 nucleotides 1 to 500 of SEQ ID NO:47,
 nucleotides 1 to 500 of SEQ ID NO:49,
 30 nucleotides 1 to 500 of SEQ ID NO:51,
 nucleotides 1 to 500 of SEQ ID NO:53,
 nucleotides 1 to 500 of SEQ ID NO:55,
 nucleotides 1 to 500 of SEQ ID NO:57,
 nucleotides 1 to 500 of SEQ ID NO:59,
 35 nucleotides 1 to 500 of SEQ ID NO:65,
 nucleotides 1 to 221 of SEQ ID NO:17,
 nucleotides 1 to 239 of SEQ ID NO:18,

- nucleotides 1 to 199 of SEQ ID NO:19,
 nucleotides 1 to 191 of SEQ ID NO:20,
 nucleotides 1 to 232 of SEQ ID NO:21,
 nucleotides 1 to 467 of SEQ ID NO:22,
 5 nucleotides 1 to 534 of SEQ ID NO:23,
 nucleotides 1 to 563 of SEQ ID NO:24,
 nucleotides 1 to 218 of SEQ ID NO:25,
 nucleotides 1 to 492 of SEQ ID NO:26,
 nucleotides 1 to 481 of SEQ ID NO:27,
 10 nucleotides 1 to 463 of SEQ ID NO:28,
 nucleotides 1 to 513 of SEQ ID NO:29,
 nucleotides 1 to 579 of SEQ ID NO:30,
 nucleotides 1 to 514 of SEQ ID NO:31,
 nucleotides 1 to 477 of SEQ ID NO:32,
 15 nucleotides 1 to 500 of SEQ ID NO:33,
 nucleotides 1 to 470 of SEQ ID NO:34,
 nucleotides 1 to 491 of SEQ ID NO:35,
 nucleotides 1 to 221 of SEQ ID NO:36,
 nucleotides 1 to 519 of SEQ ID NO:61,
 20 nucleotides 1 to 497 of SEQ ID NO:62,
 nucleotides 1 to 498 of SEQ ID NO:63,
 nucleotides 1 to 525 of SEQ ID NO:64, and
 nucleotides 1 to 951 of SEQ ID NO:67; and
 (iii) the complementary strand of the nucleotides selected from the group consisting of:
 25 nucleotides 1 to 200 of SEQ ID NO:1,
 nucleotides 1 to 200 of SEQ ID NO:3,
 nucleotides 1 to 200 of SEQ ID NO:5,
 nucleotides 1 to 200 of SEQ ID NO:7,
 nucleotides 1 to 200 of SEQ ID NO:9,
 30 nucleotides 1 to 200 of SEQ ID NO:11,
 nucleotides 1 to 200 of SEQ ID NO:13,
 nucleotides 1 to 200 of SEQ ID NO:15,
 nucleotides 1 to 200 of SEQ ID NO:37,
 nucleotides 1 to 200 of SEQ ID NO:39,
 35 nucleotides 1 to 200 of SEQ ID NO:41,
 nucleotides 1 to 200 of SEQ ID NO:43,
 nucleotides 1 to 200 of SEQ ID NO:45,

- nucleotides 1 to 200 of SEQ ID NO:47,
nucleotides 1 to 200 of SEQ ID NO:49,
nucleotides 1 to 200 of SEQ ID NO:51,
nucleotides 1 to 200 of SEQ ID NO:53,
5 nucleotides 1 to 200 of SEQ ID NO:55,
nucleotides 1 to 200 of SEQ ID NO:57,
nucleotides 1 to 200 of SEQ ID NO:59, and
nucleotides 1 to 200 of SEQ ID NO:65.
- 10 20. A polynucleotide comprising a modified nucleotide sequence selected from the group consisting of:
the nucleotide sequence of SEQ ID NO:1 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 526 of SEQ ID NO:2,
15 the nucleotide sequence of SEQ ID NO:3 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 529 of SEQ ID NO:4,
the nucleotide sequence of SEQ ID NO:5 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 451
20 of SEQ ID NO:6,
the nucleotide sequence of SEQ ID NO:7 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 457 of SEQ ID NO:8,
the nucleotide sequence of SEQ ID NO:9 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 538
25 of SEQ ID NO:10,
the nucleotide sequence of SEQ ID NO:11 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 415 of SEQ ID NO:12,
30 the nucleotide sequence of SEQ ID NO:13 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 447 of SEQ ID NO:14,
the nucleotide sequence of SEQ ID NO:15 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 452
35 of SEQ ID NO:16,
the nucleotide sequence of SEQ ID NO:37 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 454

of SEQ ID NO:38,

the nucleotide sequence of SEQ ID NO:39 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 458 of SEQ ID NO:40,

5 the nucleotide sequence of SEQ ID NO:41 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 450 of SEQ ID NO:42,

the nucleotide sequence of SEQ ID NO:43 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 446

10 of SEQ ID NO:44,

the nucleotide sequence of SEQ ID NO:45 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 527 of SEQ ID NO:46,

the nucleotide sequence of SEQ ID NO:47 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 455 of SEQ ID NO:48,

15 the nucleotide sequence of SEQ ID NO:49 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 464 of SEQ ID NO:50,

20 the nucleotide sequence of SEQ ID NO:51 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 460 of SEQ ID NO:52,

the nucleotide sequence of SEQ ID NO:53 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 450

25 of SEQ ID NO:54,

the nucleotide sequence of SEQ ID NO:55 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 532 of SEQ ID NO:56,

the nucleotide sequence of SEQ ID NO:57 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 460 of SEQ ID NO:58,

30 the nucleotide sequence of SEQ ID NO:59 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 525 of SEQ ID NO:60, and

35 the nucleotide sequence of SEQ ID NO:65 comprising at least one modification, where the modified nucleotide sequence encodes a polypeptide which consists of amino acids 1 to 456 of SEQ ID NO:66.

21. A polypeptide having cellobiohydrolase I activity which is encoded by the cellobiohydrolase I encoding part of the nucleotide sequence present in a microorganism selected from the group consisting of:

- 5 a microorganism belonging to *Zygomycota*, preferably belonging to the *Mucorales*, more preferably belonging to the family *Mucoraceae* or the family *Choanephoraceae*, most preferably belonging to the genus *Rhizomucor* or the genus *Poitrasia*, in particular *Rhizomucor pusillus* or *Poitrasia circinans*,
a microorganism belonging to the *Oomycetes*, preferably belonging to the order *Pythiales*,
10 more preferably belonging to the family *Pythiaceae*, most preferably belonging to the genus *Phytophthora*, in particular *Phytophthora infestans*,
a microorganism belonging to *Auriculariales*, preferably belonging to the family *Exidiaceae*, more preferably belonging to the genus *Exidia*, most preferably *Exidia glandulosa*,
a microorganism belonging to *Xylariales*, preferably belonging to the family *Xylariaceae*, more
15 preferably belonging to the genus *Xylaria*, most preferably *Xylaria hypoxylon*,
a microorganism belonging to *Dothideales*, preferably belonging to the family *Dothideaceae*, more preferably belonging to the genus *Diplodia*, most preferably *Diplodia gossypina*,
a microorganism belonging to *Pezizales*, preferably belonging to the family *Pyronemataceae* or the family *Sarcosomataceae*, more preferably belonging to the genus *Trichophaea* or the
20 genus *Pseudoplectania*, most preferably *Trichophaea saccata* or *Pseudoplectania nigrella*,
a microorganism belonging to the family *Rigidiporaceae*, preferably belonging to the genus *Meripilus*, more preferably *Meripilus giganteus*,
a microorganism belonging to the family *Meruliaceae*, preferably belonging to the genus *Sporothrichum*, more preferably *Sporothrichum pruinosum*,
25 a microorganism belonging to the family *Agaricaceae* (under *Basidiomycota*, *Hymenomycetes*, *Agaricales*), more preferably belonging to the genus *Coprinus*, most preferably *Coprinus cinereus*,
a microorganism belonging to the family *Hypocreaceae*, preferably belonging to the genus *Acremonium* or the genus *Verticillium*, more preferably *Acremonium thermophilum* or
30 *Verticillium tenerum*,
a microorganism belonging to the genus *Cladorrhinum*, preferably *Cladorrhinum foecundissimum*,
a microorganism belonging to the genus *Myceliophthora*, preferably *Myceliophthora thermophila* or *Myceliophthora hinnulea*,
35 a microorganism belonging to the genus *Chaetomium*, preferably *Chaetomium thermophilum*,
a microorganism belonging to the genus *Chaetomidium*, preferably *Chaetomidium pingtungium*,

a microorganism belonging to the genus *Thielavia*, preferably *Thielavia australiensis* or *Thielavia microspora*,

a microorganism belonging to the genus *Thermoascus*, preferably *Thermoascus aurantiacus*,

a microorganism belonging to the genus *Trichothecium*, preferably *Trichothecium roseum*, and

5 a microorganism belonging to the species *Humicola nigrescens*.

22. A method for shuffling of DNA comprising using the polynucleotide as defined in any of claims 9 and 16-20.

10 23. A polynucleotide encoding a polypeptide having cellobiase activity obtainable by the method of claim 22.

24. A polypeptide having cellobiase activity encoded by the polynucleotide of claim 23.

15 25. Use of the polynucleotide as defined in any of claims 9 and 16-20 for DNA shuffling.

26. A method for producing ethanol from biomass, comprising contacting the biomass with the polypeptide as defined in any of claims 1-8.

20 27. Use of the polypeptide as defined in any of claims 1-8 for producing ethanol.

28. A transgenic plant, plant part or plant cell, which has been transformed with a nucleotide sequence encoding a polypeptide having cellobiohydrolase I activity as defined in any of claims 1- 8.

25

29. A detergent composition comprising a surfactant and the polypeptide according to any of claims 1-8.

SEQUENCE LISTING

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<120> Polypeptides having cellobiohydrolase I activity and polynucleotides encoding same

<130> 10129-WO

<160> 67

<170> PatentIn version 3.1

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Ala	Gln	Gln	Ala	Cys	Thr	Leu	Thr	Ala	Glu	Asn	His	Pro	Thr	Leu	Ser	
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ttc	acc	ttc	gac	gtg	gac	gtc	aca	ggc	ctc	ggc	tgc	ggt	ctg	aac	ggc	480
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Ser	Gly	Asn	Lys	Ala	Gly	Ala	Lys	Tyr	Gly	Thr	Gly	Tyr	Cys	Asp	Ser	
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Gln	Cys	Pro	Arg	Asp	Leu	Lys	Phe	Ile	Asn	Gly	Glu	Ala	Asn	Asn	Val	
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Glu	Gly	Asp	Asp	Cys	Gly	Gly	Thr	Tyr	Ser	Thr	Asp	Arg	Tyr	Ala	Gly	
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Thr	Thr	Phe	Tyr	Gly	Lys	Gly	Met	Thr	Val	Asp	Thr	Ser	Lys	Lys	Phe	
	290					295					300					
acg	gtg	gtg	acc	cag	ttc	ctg	acg	gac	tcg	tct	ggc	aac	ctg	tcc	gag	960
Thr	Val	Val	Thr	Gln	Phe	Leu	Thr	Asp	Ser	Ser	Gly	Asn	Leu	Ser	Glu	
	305				310					315					320	
atc	aag	cgc	ttc	tac	gtc	cag	aac	ggc	gtc	gtc	att	ccc	aac	tcg	aac	1008
Ile	Lys	Arg	Phe	Tyr	Val	Gln	Asn	Gly	Val	Val	Ile	Pro	Asn	Ser	Asn	
				325					330					335		
tcc	aac	atc	gcg	ggc	gtc	tcg	ggc	aac	tcc	atc	acc	cag	gcc	ttc	tgc	1056
Ser	Asn	Ile	Ala	Gly	Val	Ser	Gly	Asn	Ser	Ile	Thr	Gln	Ala	Phe	Cys	
			340					345					350			
gat	gct	cag	aag	acc	gct	ttc	ggc	gac	acc	aac	gtc	ttc	gac	caa	aag	1104
Asp	Ala	Gln	Lys	Thr	Ala	Phe	Gly	Asp	Thr	Asn	Val	Phe	Asp	Gln	Lys	
		355					360					365				
ggc	ggc	ctg	gcc	cag	atg	ggc	aag	gct	ctt	gcc	cag	ccc	atg	gtc	ctc	1152
Gly	Gly	Leu	Ala	Gln	Met	Gly	Lys	Ala	Leu	Ala	Gln	Pro	Met	Val	Leu	
	370					375					380					
gtc	atg	tcc	ctc	tgg	gac	gac	cac	gcc	gtc	aac	atg	ctc	tgg	ctc	gac	1200
Val	Met	Ser	Leu	Trp	Asp	Asp	His	Ala	Val	Asn	Met	Leu	Trp	Leu	Asp	
	385				390					395					400	

tcg acc tac ccg acc aac gcg gcc ggc aag ccg ggc gcc gcc cgc ggt 1248
 Ser Thr Tyr Pro Thr Asn Ala Ala Gly Lys Pro Gly Ala Ala Arg Gly
 405 410 415

acc tgc ccc acc acc tcg ggc gtc ccc gcc gac gtc gag tcc cag gcg 1296
 Thr Cys Pro Thr Thr Ser Gly Val Pro Ala Asp Val Glu Ser Gln Ala
 420 425 430

ccc aac tcc aag gtc atc tac tcc aac atc cgc ttc ggc ccc atc ggc 1344
 Pro Asn Ser Lys Val Ile Tyr Ser Asn Ile Arg Phe Gly Pro Ile Gly
 435 440 445

tcc acc gtc tcc ggc ctg ccc ggc ggc ggc agc aac ccc ggc ggc ggc 1392
 Ser Thr Val Ser Gly Leu Pro Gly Gly Gly Ser Asn Pro Gly Gly Gly
 450 455 460

tcc agc tcc acc acc acc acc acc aga ccc gcc acc tcc acc acc tcc 1440
 Ser Ser Ser Thr Thr Thr Thr Thr Arg Pro Ala Thr Ser Thr Thr Ser
 465 470 475 480

tcg gcc agc tcc ggc ccg acc ggc ggt ggc acg gct gcc cac tgg ggc 1488
 Ser Ala Ser Ser Gly Pro Thr Gly Gly Gly Thr Ala Ala His Trp Gly
 485 490 495

cag tgc ggc ggc atc ggc tgg acc ggc ccg acc gtc tgc gcc tcg ccc 1536
 Gln Cys Gly Gly Ile Gly Trp Thr Gly Pro Thr Val Cys Ala Ser Pro
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tac acc tgc cag aag ctg aac gac tgg tac tac cag tgc ctc taa 1581
 Tyr Thr Cys Gln Lys Leu Asn Asp Trp Tyr Tyr Gln Cys Leu
 515 520 525

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 <212> PRT
 <213> Acremonium thermophilum

<400> 2

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Trp Ser Lys Cys Thr Ser Gly Gly Ser Cys Thr Ser Val Ser Gly Ser
 35 40 45

Val Thr Ile Asp Ala Asn Trp Arg Trp Thr His Gln Val Ser Ser Ser
 50 55 60

Thr Asn Cys Tyr Thr Gly Asn Glu Trp Asp Thr Ser Ile Cys Thr Asp
 65 70 75 80

Gly Ala Ser Cys Ala Ala Ala Cys Cys Leu Asp Gly Ala Asp Tyr Ser
 85 90 95

Gly Thr Tyr Gly Ile Thr Thr Ser Gly Asn Ala Leu Ser Leu Gln Phe
 100 105 110

Val	Thr	Gln	Gly	Pro	Tyr	Ser	Thr	Asn	Ile	Gly	Ser	Arg	Thr	Tyr	Leu
		115					120					125			
Met	Ala	Ser	Asp	Thr	Lys	Tyr	Gln	Met	Phe	Thr	Leu	Leu	Gly	Asn	Glu
	130					135					140				
Phe	Thr	Phe	Asp	Val	Asp	Val	Thr	Gly	Leu	Gly	Cys	Gly	Leu	Asn	Gly
145					150					155					160
Ala	Leu	Tyr	Phe	Val	Ser	Met	Asp	Glu	Asp	Gly	Gly	Leu	Ser	Lys	Tyr
				165					170					175	
Ser	Gly	Asn	Lys	Ala	Gly	Ala	Lys	Tyr	Gly	Thr	Gly	Tyr	Cys	Asp	Ser
		180						185					190		
Gln	Cys	Pro	Arg	Asp	Leu	Lys	Phe	Ile	Asn	Gly	Glu	Ala	Asn	Asn	Val
		195					200					205			
Gly	Trp	Thr	Pro	Ser	Ser	Asn	Asp	Lys	Asn	Ala	Gly	Leu	Gly	Asn	Tyr
	210					215					220				
Gly	Ser	Cys	Cys	Ser	Glu	Met	Asp	Val	Trp	Glu	Ala	Asn	Ser	Ile	Ser
225					230					235					240
Ala	Ala	Tyr	Thr	Pro	His	Pro	Cys	Thr	Thr	Ile	Gly	Gln	Thr	Arg	Cys
				245					250					255	
Glu	Gly	Asp	Asp	Cys	Gly	Gly	Thr	Tyr	Ser	Thr	Asp	Arg	Tyr	Ala	Gly
			260					265					270		
Glu	Cys	Asp	Pro	Asp	Gly	Cys	Asp	Phe	Asn	Ser	Tyr	Arg	Met	Gly	Asn
		275					280					285			
Thr	Thr	Phe	Tyr	Gly	Lys	Gly	Met	Thr	Val	Asp	Thr	Ser	Lys	Lys	Phe
	290					295					300				
Thr	Val	Val	Thr	Gln	Phe	Leu	Thr	Asp	Ser	Ser	Gly	Asn	Leu	Ser	Glu
305				310						315					320
Ile	Lys	Arg	Phe	Tyr	Val	Gln	Asn	Gly	Val	Val	Ile	Pro	Asn	Ser	Asn
				325					330					335	
Ser	Asn	Ile	Ala	Gly	Val	Ser	Gly	Asn	Ser	Ile	Thr	Gln	Ala	Phe	Cys
			340					345					350		
Asp	Ala	Gln	Lys	Thr	Ala	Phe	Gly	Asp	Thr	Asn	Val	Phe	Asp	Gln	Lys
		355					360					365			
Gly	Gly	Leu	Ala	Gln	Met	Gly	Lys	Ala	Leu	Ala	Gln	Pro	Met	Val	Leu
	370					375					380				
Val	Met	Ser	Leu	Trp	Asp	Asp	His	Ala	Val	Asn	Met	Leu	Trp	Leu	Asp
385					390					395					400
Ser	Thr	Tyr	Pro	Thr	Asn	Ala	Ala	Gly	Lys	Pro	Gly	Ala	Ala	Arg	Gly
				405					410					415	
Thr	Cys	Pro	Thr	Thr	Ser	Gly	Val	Pro	Ala	Asp	Val	Glu	Ser	Gln	Ala
			420					425					430		
Pro	Asn	Ser	Lys	Val	Ile	Tyr	Ser	Asn	Ile	Arg	Phe	Gly	Pro	Ile	Gly
	435						440					445			

Ser Thr Val Ser Gly Leu Pro Gly Gly Gly Ser Asn Pro Gly Gly Gly
 450 455 460

Ser Ser Ser Thr Thr Thr Thr Thr Arg Pro Ala Thr Ser Thr Thr Ser
 465 470 475 480

Ser Ala Ser Ser Gly Pro Thr Gly Gly Gly Thr Ala Ala His Trp Gly
 485 490 495

Gln Cys Gly Gly Ile Gly Trp Thr Gly Pro Thr Val Cys Ala Ser Pro
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Tyr Thr Cys Gln Lys Leu Asn Asp Trp Tyr Tyr Gln Cys Leu
 515 520 525

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 <213> Chaetomium thermophilum

<220>
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 <222> (1)..(1590)
 <223>

<400> 3

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gcc gcc cag cag gct tgc tcc ctc acc act gag acc cac ccc aga ctc	96
Ala Ala Gln Gln Ala Cys Ser Leu Thr Thr Glu Thr His Pro Arg Leu	
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act tgg aag cgc tgc acc tct ggc ggc aac tgc tcg acc gtg aac ggc	144
Thr Trp Lys Arg Cys Thr Ser Gly Gly Asn Cys Ser Thr Val Asn Gly	
35 40 45	
gcc gtc acc atc gat gcc aac tgg cgc tgg act cac acc gtt tcc ggc	192
Ala Val Thr Ile Asp Ala Asn Trp Arg Trp Thr His Thr Val Ser Gly	
50 55 60	
tcg acc aac tgc tac acc ggc aac gag tgg gat acc tcc atc tgc tct	240
Ser Thr Asn Cys Tyr Thr Gly Asn Glu Trp Asp Thr Ser Ile Cys Ser	
65 70 75 80	
gat ggc aag agc tgc gcc cag acc tgc tgc gtc gac ggc gct gac tac	288
Asp Gly Lys Ser Cys Ala Gln Thr Cys Cys Val Asp Gly Ala Asp Tyr	
85 90 95	
tct tcg acc tat ggt atc acc acc agc ggt gac tcc ctg aac ctc aag	336
Ser Ser Thr Tyr Gly Ile Thr Thr Ser Gly Asp Ser Leu Asn Leu Lys	
100 105 110	
ttc gtc acc aag cac cag tac ggc acc aat gtc ggc tct cgt gtc tac	384
Phe Val Thr Lys His Gln Tyr Gly Thr Asn Val Gly Ser Arg Val Tyr	
115 120 125	
ctg atg gag aac gac acc aag tac cag atg ttc gag ctc ctc ggc aac	432

Leu	Met	Glu	Asn	Asp	Thr	Lys	Tyr	Gln	Met	Phe	Glu	Leu	Leu	Gly	Asn	
130						135					140					
gag	ttc	acc	ttc	gat	gtc	gat	gtc	tct	aac	ctg	ggc	tgc	ggc	ctc	aac	480
Glu	Phe	Thr	Phe	Asp	Val	Asp	Val	Ser	Asn	Leu	Gly	Cys	Gly	Leu	Asn	
145					150					155					160	
ggc	gcc	ctc	tac	ttc	gtc	tcc	atg	gac	gct	gat	ggc	ggc	atg	agc	aag	528
Gly	Ala	Leu	Tyr	Phe	Val	Ser	Met	Asp	Ala	Asp	Gly	Gly	Met	Ser	Lys	
				165					170					175		
tac	tct	ggc	aac	aag	gct	ggc	gcc	aag	tac	ggg	acg	ggg	tac	tgt	gat	576
Tyr	Ser	Gly	Asn	Lys	Ala	Gly	Ala	Lys	Tyr	Gly	Thr	Gly	Tyr	Cys	Asp	
			180					185					190			
gct	cag	tgc	ccg	cgc	gac	ctt	aag	ttc	atc	aac	ggc	gag	gcc	aac	att	624
Ala	Gln	Cys	Pro	Arg	Asp	Leu	Lys	Phe	Ile	Asn	Gly	Glu	Ala	Asn	Ile	
		195					200					205				
gag	aac	tgg	acc	cct	tcg	acc	aat	gat	gcc	aac	gcc	ggc	ttc	ggc	cgc	672
Glu	Asn	Trp	Thr	Pro	Ser	Thr	Asn	Asp	Ala	Asn	Ala	Gly	Phe	Gly	Arg	
	210					215					220					
tat	ggc	agc	tgc	tgc	tct	gag	atg	gat	atc	tgg	gag	gcc	aac	aac	atg	720
Tyr	Gly	Ser	Cys	Cys	Ser	Glu	Met	Asp	Ile	Trp	Glu	Ala	Asn	Asn	Met	
225					230					235					240	
gct	act	gcc	ttc	act	cct	cac	cct	tgc	acc	att	atc	ggc	cag	agc	cgc	768
Ala	Thr	Ala	Phe	Thr	Pro	His	Pro	Cys	Thr	Ile	Ile	Gly	Gln	Ser	Arg	
				245					250					255		
tgc	gag	ggc	aac	agc	tgc	ggc	ggc	acc	tac	agc	tct	gag	cgc	tat	gct	816
Cys	Glu	Gly	Asn	Ser	Cys	Gly	Gly	Thr	Tyr	Ser	Ser	Glu	Arg	Tyr	Ala	
			260					265					270			
ggc	gtt	tgc	gat	cct	gat	ggc	tgc	gac	ttc	aac	gcc	tac	cgc	cag	ggc	864
Gly	Val	Cys	Asp	Pro	Asp	Gly	Cys	Asp	Phe	Asn	Ala	Tyr	Arg	Gln	Gly	
		275					280					285				
gac	aag	acc	ttc	tac	ggc	aag	ggc	atg	acc	gtc	gac	acc	acc	aag	aag	912
Asp	Lys	Thr	Phe	Tyr	Gly	Lys	Gly	Met	Thr	Val	Asp	Thr	Thr	Lys	Lys	
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atg	acc	gtc	gtc	acc	cag	ttc	cac	aag	aac	tcg	gct	ggc	gtc	ctc	agc	960
Met	Thr	Val	Val	Thr	Gln	Phe	His	Lys	Asn	Ser	Ala	Gly	Val	Leu	Ser	
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gag	atc	aag	cgc	ttc	tac	gtt	cag	gac	ggc	aag	gtc	att	gcc	aac	gcc	1008
Glu	Ile	Lys	Arg	Phe	Tyr	Val	Gln	Asp	Gly	Lys	Val	Ile	Ala	Asn	Ala	
				325					330					335		
gag	tcc	aag	atc	ccc	ggc	aac	ccc	ggc	aac	tcc	atc	acc	cag	gag	tgg	1056
Glu	Ser	Lys	Ile	Pro	Gly	Asn	Pro	Gly	Asn	Ser	Ile	Thr	Gln	Glu	Trp	
			340					345					350			
tgc	gat	gcc	cag	aag	gtc	gcc	ttc	ggc	gac	atc	gat	gac	ttc	aac	cgc	1104
Cys	Asp	Ala	Gln	Lys	Val	Ala	Phe	Gly	Asp	Ile	Asp	Asp	Phe	Asn	Arg	
		355					360				365					
aag	ggc	ggc	atg	gct	cag	atg	agc	aag	gcc	ctc	gaa	ggc	cct	atg	gtc	1152
Lys	Gly	Gly	Met	Ala	Gln	Met	Ser	Lys	Ala	Leu	Glu	Gly	Pro	Met	Val	
	370					375					380					

ctg gtc atg tcc gtc tgg gat gac cac tac gcc aac atg ctc tgg ctc 1200
 Leu Val Met Ser Val Trp Asp Asp His Tyr Ala Asn Met Leu Trp Leu
 385 390 395 400

gac tcg acc tac ccc atc gac aag gcc ggc acc ccc ggc gcc gag cgc 1248
 Asp Ser Thr Tyr Pro Ile Asp Lys Ala Gly Thr Pro Gly Ala Glu Arg
 405 410 415

ggt gct tgc ccg acc acc tcc ggt gtc cct gcc gag att gag gcc cag 1296
 Gly Ala Cys Pro Thr Thr Ser Gly Val Pro Ala Glu Ile Glu Ala Gln
 420 425 430

gtc ccc aac agc aac gtc atc ttc tcc aac atc cgc ttc ggc ccc atc 1344
 Val Pro Asn Ser Asn Val Ile Phe Ser Asn Ile Arg Phe Gly Pro Ile
 435 440 445

ggc tcg acc gtc cct ggc ctc gac ggc agc act ccc agc aac ccg acc 1392
 Gly Ser Thr Val Pro Gly Leu Asp Gly Ser Thr Pro Ser Asn Pro Thr
 450 455 460

gcc acc gtt gct cct ccc act tct acc acc agc gtg aga agc agc act 1440
 Ala Thr Val Ala Pro Pro Thr Ser Thr Thr Ser Val Arg Ser Ser Thr
 465 470 475 480

act cag att tcc acc ccg act agc cag ccc ggc ggc tgc acc acc cag 1488
 Thr Gln Ile Ser Thr Pro Thr Ser Gln Pro Gly Gly Cys Thr Thr Gln
 485 490 495

aag tgg ggc cag tgc ggt ggt atc ggc tac acc ggc tgc act aac tgc 1536
 Lys Trp Gly Gln Cys Gly Gly Ile Gly Tyr Thr Gly Cys Thr Asn Cys
 500 505 510

gtt gct ggc act acc tgc act gag ctc aac ccc tgg tac agc cag tgc 1584
 Val Ala Gly Thr Thr Cys Thr Glu Leu Asn Pro Trp Tyr Ser Gln Cys
 515 520 525

ctg taa 1590
 Leu

<210> 4
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 <212> PRT
 <213> Chaetomium thermophilum

<400> 4

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Thr Trp Lys Arg Cys Thr Ser Gly Gly Asn Cys Ser Thr Val Asn Gly
 35 40 45

Ala Val Thr Ile Asp Ala Asn Trp Arg Trp Thr His Thr Val Ser Gly
 50 55 60

Ser Thr Asn Cys Tyr Thr Gly Asn Glu Trp Asp Thr Ser Ile Cys Ser

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Asp Gly Lys Ser Cys Ala Gln Thr Cys Cys Val Asp Gly Ala Asp Tyr						
		85		90		95
Ser Ser Thr Tyr Gly Ile Thr Thr Ser Gly Asp Ser Leu Asn Leu Lys						
		100		105		110
Phe Val Thr Lys His Gln Tyr Gly Thr Asn Val Gly Ser Arg Val Tyr						
		115		120		125
Leu Met Glu Asn Asp Thr Lys Tyr Gln Met Phe Glu Leu Leu Gly Asn						
		130		135		140
Glu Phe Thr Phe Asp Val Asp Val Ser Asn Leu Gly Cys Gly Leu Asn						
		145		150		155
Gly Ala Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Met Ser Lys						
		165		170		175
Tyr Ser Gly Asn Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp						
		180		185		190
Ala Gln Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Glu Ala Asn Ile						
		195		200		205
Glu Asn Trp Thr Pro Ser Thr Asn Asp Ala Asn Ala Gly Phe Gly Arg						
		210		215		220
Tyr Gly Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Asn Met						
		225		230		235
Ala Thr Ala Phe Thr Pro His Pro Cys Thr Ile Ile Gly Gln Ser Arg						
		245		250		255
Cys Glu Gly Asn Ser Cys Gly Gly Thr Tyr Ser Ser Glu Arg Tyr Ala						
		260		265		270
Gly Val Cys Asp Pro Asp Gly Cys Asp Phe Asn Ala Tyr Arg Gln Gly						
		275		280		285
Asp Lys Thr Phe Tyr Gly Lys Gly Met Thr Val Asp Thr Thr Lys Lys						
		290		295		300
Met Thr Val Val Thr Gln Phe His Lys Asn Ser Ala Gly Val Leu Ser						
		305		310		315
Glu Ile Lys Arg Phe Tyr Val Gln Asp Gly Lys Val Ile Ala Asn Ala						
		325		330		335
Glu Ser Lys Ile Pro Gly Asn Pro Gly Asn Ser Ile Thr Gln Glu Trp						
		340		345		350
Cys Asp Ala Gln Lys Val Ala Phe Gly Asp Ile Asp Asp Phe Asn Arg						
		355		360		365
Lys Gly Gly Met Ala Gln Met Ser Lys Ala Leu Glu Gly Pro Met Val						
		370		375		380
Leu Val Met Ser Val Trp Asp Asp His Tyr Ala Asn Met Leu Trp Leu						
		385		390		395
						400

Asp Ser Thr Tyr Pro Ile Asp Lys Ala Gly Thr Pro Gly Ala Glu Arg
 405 410 415
 Gly Ala Cys Pro Thr Thr Ser Gly Val Pro Ala Glu Ile Glu Ala Gln
 420 425 430
 Val Pro Asn Ser Asn Val Ile Phe Ser Asn Ile Arg Phe Gly Pro Ile
 435 440 445
 Gly Ser Thr Val Pro Gly Leu Asp Gly Ser Thr Pro Ser Asn Pro Thr
 450 455 460
 Ala Thr Val Ala Pro Pro Thr Ser Thr Thr Ser Val Arg Ser Ser Thr
 465 470 475 480
 Thr Gln Ile Ser Thr Pro Thr Ser Gln Pro Gly Gly Cys Thr Thr Gln
 485 490 495
 Lys Trp Gly Gln Cys Gly Gly Ile Gly Tyr Thr Gly Cys Thr Asn Cys
 500 505 510
 Val Ala Gly Thr Thr Cys Thr Glu Leu Asn Pro Trp Tyr Ser Gln Cys
 515 520 525

Leu

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 <212> DNA
 <213> Scytalidium sp.

<220>
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 <222> (1)..(1356)
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<400> 5

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ctg agc agc gtc gct gcc cag cag gcc ggc acc atc acc gcc gag aac	96
Leu Ser Ser Val Ala Ala Gln Gln Ala Gly Thr Ile Thr Ala Glu Asn	
20 25 30	
cac ccc agg atg acc tgg aag agg tgc tcg ggc ccc ggc aac tgc cag	144
His Pro Arg Met Thr Trp Lys Arg Cys Ser Gly Pro Gly Asn Cys Gln	
35 40 45	
acc gtg cag ggc gag gtc gtc atc gac gcc aac tgg cgc tgg ctg cac	192
Thr Val Gln Gly Glu Val Val Ile Asp Ala Asn Trp Arg Trp Leu His	
50 55 60	
aac aac ggc cag aac tgc tat gag ggc aac aag tgg acc agc cag tgc	240
Asn Asn Gly Gln Asn Cys Tyr Glu Gly Asn Lys Trp Thr Ser Gln Cys	
65 70 75 80	
agc tcg gcc acc gac tgc gcg cag agg tgc gcc ctc gac ggt gcc aac	288
Ser Ser Ala Thr Asp Cys Ala Gln Arg Cys Ala Leu Asp Gly Ala Asn	

85				90				95								
tac	cag	tcg	acc	tac	ggc	gcc	tcg	acc	agc	ggc	gac	tcc	ctg	acg	ctc	336
Tyr	Gln	Ser	Thr	Tyr	Gly	Ala	Ser	Thr	Ser	Gly	Asp	Ser	Leu	Thr	Leu	
100				105				110								
aag	ttc	gtc	acc	aag	cac	gag	tac	ggc	acc	aac	atc	ggc	tcg	cgc	ttc	384
Lys	Phe	Val	Thr	Lys	His	Glu	Tyr	Gly	Thr	Asn	Ile	Gly	Ser	Arg	Phe	
115				120				125								
tac	ctc	atg	gcc	aac	cag	aac	aag	tac	cag	atg	ttc	acc	ctg	atg	aac	432
Tyr	Leu	Met	Ala	Asn	Gln	Asn	Lys	Tyr	Gln	Met	Phe	Thr	Leu	Met	Asn	
130				135				140								
aac	gag	ttc	gcc	ttc	gat	gtc	gac	ctc	tcc	aag	gtt	gag	tgc	ggc	atc	480
Asn	Glu	Phe	Ala	Phe	Asp	Val	Asp	Leu	Ser	Lys	Val	Glu	Cys	Gly	Ile	
145				150				155				160				
aac	agc	gct	ctg	tac	ttc	gtc	gcc	atg	gag	gag	gat	ggc	ggc	atg	gcc	528
Asn	Ser	Ala	Leu	Tyr	Phe	Val	Ala	Met	Glu	Glu	Asp	Gly	Gly	Met	Ala	
165				170				175								
agc	tac	ccg	agc	aac	cgt	gct	ggc	gcc	aag	tac	ggc	acg	ggc	tac	tgc	576
Ser	Tyr	Pro	Ser	Asn	Arg	Ala	Gly	Ala	Lys	Tyr	Gly	Thr	Gly	Tyr	Cys	
180				185				190								
gat	gcc	caa	tgc	gcc	cgt	gac	ctc	aag	ttc	att	ggc	ggc	aag	gcc	aac	624
Asp	Ala	Gln	Cys	Ala	Arg	Asp	Leu	Lys	Phe	Ile	Gly	Gly	Lys	Ala	Asn	
195				200				205								
att	gag	ggc	tgg	cgc	ccg	tcc	acc	aac	gac	ccc	aac	gcc	ggc	gtc	ggc	672
Ile	Glu	Gly	Trp	Arg	Pro	Ser	Thr	Asn	Asp	Pro	Asn	Ala	Gly	Val	Gly	
210				215				220								
ccc	atg	ggc	gcc	tgc	tgc	gct	gag	atc	gac	gtt	tgg	gag	tcc	aac	gcc	720
Pro	Met	Gly	Ala	Cys	Cys	Ala	Glu	Ile	Asp	Val	Trp	Glu	Ser	Asn	Ala	
225				230				235				240				
tat	gct	tat	gcc	ttc	acc	ccc	cac	gcc	tgc	ggc	agc	aag	aac	cgc	tac	768
Tyr	Ala	Tyr	Ala	Phe	Thr	Pro	His	Ala	Cys	Gly	Ser	Lys	Asn	Arg	Tyr	
245				250				255								
cac	atc	tgc	gag	acc	aac	aac	tgc	ggc	ggc	acc	tac	tcg	gat	gac	cgc	816
His	Ile	Cys	Glu	Thr	Asn	Asn	Cys	Gly	Gly	Thr	Tyr	Ser	Asp	Asp	Arg	
260				265				270								
ttc	gcc	ggc	tac	tgc	gac	gcc	aac	ggc	tgc	gac	tac	aac	ccc	tac	cgc	864
Phe	Ala	Gly	Tyr	Cys	Asp	Ala	Asn	Gly	Cys	Asp	Tyr	Asn	Pro	Tyr	Arg	
275				280				285								
atg	ggc	aac	aag	gac	ttc	tat	ggc	aag	ggc	aag	acc	gtc	gac	acc	aac	912
Met	Gly	Asn	Lys	Asp	Phe	Tyr	Gly	Lys	Gly	Lys	Thr	Val	Asp	Thr	Asn	
290				295				300								
cgc	aag	ttc	acc	gtt	gtc	tcc	cgc	ttc	gag	cgt	aac	agg	ctc	tct	cag	960
Arg	Lys	Phe	Thr	Val	Val	Ser	Arg	Phe	Glu	Arg	Asn	Arg	Leu	Ser	Gln	
305				310				315				320				
ttc	ttc	gtc	cag	gac	ggc	cgc	aag	atc	gag	gtg	ccc	cct	ccg	acc	tgg	1008
Phe	Phe	Val	Gln	Asp	Gly	Arg	Lys	Ile	Glu	Val	Pro	Pro	Pro	Thr	Trp	
325				330				335								

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ccc ggc ctc ccg aac agc gcc gac atc acc cct gag ctc tgc gat gct      1056
Pro Gly Leu Pro Asn Ser Ala Asp Ile Thr Pro Glu Leu Cys Asp Ala
          340                      345                      350

cag ttc cgc gtc ttc gat gac cgc aac cgc ttc gcc gag acc ggt ggc      1104
Gln Phe Arg Val Phe Asp Asp Arg Asn Arg Phe Ala Glu Thr Gly Gly
          355                      360                      365

ttc gat gct ctg aac gag gcc ctc acc att ccc atg gtc ctt gtc atg      1152
Phe Asp Ala Leu Asn Glu Ala Leu Thr Ile Pro Met Val Leu Val Met
          370                      375                      380

tcc atc tgg gat gac cac cac tcc aac atg ctc tgg ctc gac tcc agc      1200
Ser Ile Trp Asp Asp His His Ser Asn Met Leu Trp Leu Asp Ser Ser
          385                      390                      395                      400

tac ccg ccc gag aag gcc ggc ctc ccc ggt ggc gac cgt ggc ccg tgc      1248
Tyr Pro Pro Glu Lys Ala Gly Leu Pro Gly Gly Asp Arg Gly Pro Cys
          405                      410                      415

ccg acc acc tct ggt gtc cct gcc gag gtc gag gct cag tac ccc gat      1296
Pro Thr Thr Ser Gly Val Pro Ala Glu Val Glu Ala Gln Tyr Pro Asp
          420                      425                      430

gct cag gtc gtc tgg tcc aac atc cgc ttc ggc ccc atc ggc tcg acc      1344
Ala Gln Val Val Trp Ser Asn Ile Arg Phe Gly Pro Ile Gly Ser Thr
          435                      440                      445

gtc aac gtc taa
Val Asn Val
          450

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<210> 6
<211> 451
<212> PRT
<213> Scytalidium sp.

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<400> 6

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Met Gln Ile Lys Ser Tyr Ile Gln Tyr Leu Ala Ala Ala Leu Pro Leu
1          5          10          15

Leu Ser Ser Val Ala Ala Gln Gln Ala Gly Thr Ile Thr Ala Glu Asn
          20          25          30

His Pro Arg Met Thr Trp Lys Arg Cys Ser Gly Pro Gly Asn Cys Gln
          35          40          45

Thr Val Gln Gly Glu Val Val Ile Asp Ala Asn Trp Arg Trp Leu His
          50          55          60

Asn Asn Gly Gln Asn Cys Tyr Glu Gly Asn Lys Trp Thr Ser Gln Cys
65          70          75          80

Ser Ser Ala Thr Asp Cys Ala Gln Arg Cys Ala Leu Asp Gly Ala Asn
          85          90          95

Tyr Gln Ser Thr Tyr Gly Ala Ser Thr Ser Gly Asp Ser Leu Thr Leu
          100          105          110

Lys Phe Val Thr Lys His Glu Tyr Gly Thr Asn Ile Gly Ser Arg Phe

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115	120	125
Tyr Leu Met Ala Asn Gln Asn Lys Tyr Gln Met Phe Thr Leu Met Asn 130 135 140		
Asn Glu Phe Ala Phe Asp Val Asp Leu Ser Lys Val Glu Cys Gly Ile 145 150 155 160		
Asn Ser Ala Leu Tyr Phe Val Ala Met Glu Glu Asp Gly Gly Met Ala 165 170 175		
Ser Tyr Pro Ser Asn Arg Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys 180 185 190		
Asp Ala Gln Cys Ala Arg Asp Leu Lys Phe Ile Gly Gly Lys Ala Asn 195 200 205		
Ile Glu Gly Trp Arg Pro Ser Thr Asn Asp Pro Asn Ala Gly Val Gly 210 215 220		
Pro Met Gly Ala Cys Cys Ala Glu Ile Asp Val Trp Glu Ser Asn Ala 225 230 235 240		
Tyr Ala Tyr Ala Phe Thr Pro His Ala Cys Gly Ser Lys Asn Arg Tyr 245 250 255		
His Ile Cys Glu Thr Asn Asn Cys Gly Gly Thr Tyr Ser Asp Asp Arg 260 265 270		
Phe Ala Gly Tyr Cys Asp Ala Asn Gly Cys Asp Tyr Asn Pro Tyr Arg 275 280 285		
Met Gly Asn Lys Asp Phe Tyr Gly Lys Gly Lys Thr Val Asp Thr Asn 290 295 300		
Arg Lys Phe Thr Val Val Ser Arg Phe Glu Arg Asn Arg Leu Ser Gln 305 310 315 320		
Phe Phe Val Gln Asp Gly Arg Lys Ile Glu Val Pro Pro Pro Thr Trp 325 330 335		
Pro Gly Leu Pro Asn Ser Ala Asp Ile Thr Pro Glu Leu Cys Asp Ala 340 345 350		
Gln Phe Arg Val Phe Asp Asp Arg Asn Arg Phe Ala Glu Thr Gly Gly 355 360 365		
Phe Asp Ala Leu Asn Glu Ala Leu Thr Ile Pro Met Val Leu Val Met 370 375 380		
Ser Ile Trp Asp Asp His His Ser Asn Met Leu Trp Leu Asp Ser Ser 385 390 395 400		
Tyr Pro Pro Glu Lys Ala Gly Leu Pro Gly Gly Asp Arg Gly Pro Cys 405 410 415		
Pro Thr Thr Ser Gly Val Pro Ala Glu Val Glu Ala Gln Tyr Pro Asp 420 425 430		
Ala Gln Val Val Trp Ser Asn Ile Arg Phe Gly Pro Ile Gly Ser Thr 435 440 445		

Val Asn Val
450

<210> 7
<211> 1374
<212> DNA
<213> Thermoascus aurantiacus

<220>
<221> CDS
<222> (1)..(1374)
<223>

<400> 7

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Met Tyr Gln Arg Ala Leu Leu Phe Ser Phe Phe Leu Ser Ala Ala Arg	
1 5 10 15	
gcg cag cag gcc ggt acc cta acc gca gag aat cac cct tcc ctg acc	96
Ala Gln Gln Ala Gly Thr Leu Thr Ala Glu Asn His Pro Ser Leu Thr	
20 25 30	
tgg cag caa tgc tcc agc ggc ggt agt tgt acc acg cag aat gga aaa	144
Trp Gln Gln Cys Ser Ser Gly Gly Ser Cys Thr Thr Gln Asn Gly Lys	
35 40 45	
gtc gtt atc gat gcg aac tgg cgt tgg gtc cat acc acc tct gga tac	192
Val Val Ile Asp Ala Asn Trp Arg Trp Val His Thr Thr Ser Gly Tyr	
50 55 60	
acc aac tgc tac acg ggc aat acg tgg gac acc agt atc tgt ccc gac	240
Thr Asn Cys Tyr Thr Gly Asn Thr Trp Asp Thr Ser Ile Cys Pro Asp	
65 70 75 80	
gac gtg acc tgc gct cag aat tgt gcc ttg gat gga gcg gat tac agt	288
Asp Val Thr Cys Ala Gln Asn Cys Ala Leu Asp Gly Ala Asp Tyr Ser	
85 90 95	
ggc acc tat ggt gtt acg acc agt ggc aac gcc ctg aga ctg aac ttt	336
Gly Thr Tyr Gly Val Thr Thr Ser Gly Asn Ala Leu Arg Leu Asn Phe	
100 105 110	
gtc acc caa agc tca ggg aag aac att ggc tcg cgc ctg tac ctg ctg	384
Val Thr Gln Ser Ser Gly Lys Asn Ile Gly Ser Arg Leu Tyr Leu Leu	
115 120 125	
cag gac gac acc act tat cag atc ttc aag ctg ctg ggt cag gag ttt	432
Gln Asp Asp Thr Thr Tyr Gln Ile Phe Lys Leu Leu Gly Gln Glu Phe	
130 135 140	
acc ttc gat gtc gac gtc tcc aat ctc cct tgc ggg ctg aac ggc gcc	480
Thr Phe Asp Val Asp Val Ser Asn Leu Pro Cys Gly Leu Asn Gly Ala	
145 150 155 160	
ctc tac ttt gtg gcc atg gac gcc gac ggc gga ttg tcc aaa tac cct	528
Leu Tyr Phe Val Ala Met Asp Ala Asp Gly Gly Leu Ser Lys Tyr Pro	
165 170 175	
ggc aac aag gca ggc gct aag tat ggc act ggt tac tgc gac tct cag	576
Gly Asn Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln	

180						185						190						
tgc	cct	cgg	gat	ctc	aag	ttc	atc	aac	ggc	cag	gcc	aac	gtt	gaa	ggc	624		
Cys	Pro	Arg	Asp	Leu	Lys	Phe	Ile	Asn	Gly	Gln	Ala	Asn	Val	Glu	Gly			
195						200						205						
tgg	cag	ccg	tct	gcc	aac	gac	cca	aat	gcc	ggc	gtt	ggc	aac	cac	ggc	672		
Trp	Gln	Pro	Ser	Ala	Asn	Asp	Pro	Asn	Ala	Gly	Val	Gly	Asn	His	Gly			
210						215						220						
tcc	tgc	tgc	gct	gag	atg	gat	gtc	tgg	gaa	gcc	aac	agc	atc	tct	act	720		
Ser	Cys	Cys	Ala	Glu	Met	Asp	Val	Trp	Glu	Ala	Asn	Ser	Ile	Ser	Thr			
225						230						235						240
gcg	gtg	acg	cct	cac	cca	tgc	gac	acc	ccc	ggc	cag	acc	atg	tgc	cag	768		
Ala	Val	Thr	Pro	His	Pro	Cys	Asp	Thr	Pro	Gly	Gln	Thr	Met	Cys	Gln			
245						250						255						
gga	gac	gac	tgt	ggc	gga	acc	tac	tcc	tcc	act	cga	tat	gct	ggc	acc	816		
Gly	Asp	Asp	Cys	Gly	Gly	Thr	Tyr	Ser	Ser	Thr	Arg	Tyr	Ala	Gly	Thr			
260						265						270						
tgc	gac	cct	gat	ggc	tgc	gac	ttc	aat	cct	tac	cgc	cag	ggc	aac	cac	864		
Cys	Asp	Pro	Asp	Gly	Cys	Asp	Phe	Asn	Pro	Tyr	Arg	Gln	Gly	Asn	His			
275						280						285						
tcg	ttc	tac	ggc	ccc	ggg	aag	atc	gtc	gac	act	agc	tcc	aaa	ttc	acc	912		
Ser	Phe	Tyr	Gly	Pro	Gly	Lys	Ile	Val	Asp	Thr	Ser	Ser	Lys	Phe	Thr			
290						295						300						
gtc	gtc	acc	cag	ttc	atc	acc	gac	gac	ggg	acc	ccc	tcc	ggc	acc	ctg	960		
Val	Val	Thr	Gln	Phe	Ile	Thr	Asp	Asp	Gly	Thr	Pro	Ser	Gly	Thr	Leu			
305						310						315						320
acg	gag	atc	aaa	cgc	ttc	tac	gtc	cag	aac	ggc	aag	gtg	atc	ccc	cag	1008		
Thr	Glu	Ile	Lys	Arg	Phe	Tyr	Val	Gln	Asn	Gly	Lys	Val	Ile	Pro	Gln			
325						330						335						
tcg	gag	tcg	acg	atc	agc	ggc	gtc	acc	ggc	aac	tca	atc	acc	acc	gag	1056		
Ser	Glu	Ser	Thr	Ile	Ser	Gly	Val	Thr	Gly	Asn	Ser	Ile	Thr	Thr	Glu			
340						345						350						
tat	tgc	acg	gcc	cag	aag	gcc	gcc	ttc	ggc	gac	aac	acc	ggc	ttc	ttc	1104		
Tyr	Cys	Thr	Ala	Gln	Lys	Ala	Ala	Phe	Gly	Asp	Asn	Thr	Gly	Phe	Phe			
355						360						365						
acg	cac	ggc	ggg	ctt	cag	aag	atc	agt	cag	gct	ctg	gct	cag	ggc	atg	1152		
Thr	His	Gly	Gly	Leu	Gln	Lys	Ile	Ser	Gln	Ala	Leu	Ala	Gln	Gly	Met			
370						375						380						
gtc	ctc	gtc	atg	agc	ctg	tgg	gac	gat	cac	gcc	gcc	aac	atg	ctc	tgg	1200		
Val	Leu	Val	Met	Ser	Leu	Trp	Asp	Asp	His	Ala	Ala	Asn	Met	Leu	Trp			
385						390						395						400
ctg	gac	agc	acc	tac	ccg	act	gat	gcg	gac	ccg	gac	acc	cct	ggc	gtc	1248		
Leu	Asp	Ser	Thr	Tyr	Pro	Thr	Asp	Ala	Asp	Pro	Asp	Thr	Pro	Gly	Val			
405						410						415						
gcg	cgc	ggc	acc	tgc	ccc	acg	acc	tcc	ggc	gtc	ccg	gcc	gac	gtt	gag	1296		
Ala	Arg	Gly	Thr	Cys	Pro	Thr	Thr	Ser	Gly	Val	Pro	Ala	Asp	Val	Glu			
420						425						430						

tcg cag aac ccc aat tca tat gtt atc tac tcc aac atc aag gtc gga 1344
 Ser Gln Asn Pro Asn Ser Tyr Val Ile Tyr Ser Asn Ile Lys Val Gly
 435 440 445

ccc atc aac tcg acc ttc acc gcc aac taa 1374
 Pro Ile Asn Ser Thr Phe Thr Ala Asn
 450 455

<210> 8
 <211> 457
 <212> PRT
 <213> Thermoascus aurantiacus

<400> 8

Met Tyr Gln Arg Ala Leu Leu Phe Ser Phe Phe Leu Ser Ala Ala Arg
 1 5 10 15

Ala Gln Gln Ala Gly Thr Leu Thr Ala Glu Asn His Pro Ser Leu Thr
 20 25 30

Trp Gln Gln Cys Ser Ser Gly Gly Ser Cys Thr Thr Gln Asn Gly Lys
 35 40 45

Val Val Ile Asp Ala Asn Trp Arg Trp Val His Thr Thr Ser Gly Tyr
 50 55 60

Thr Asn Cys Tyr Thr Gly Asn Thr Trp Asp Thr Ser Ile Cys Pro Asp
 65 70 75 80

Asp Val Thr Cys Ala Gln Asn Cys Ala Leu Asp Gly Ala Asp Tyr Ser
 85 90 95

Gly Thr Tyr Gly Val Thr Thr Ser Gly Asn Ala Leu Arg Leu Asn Phe
 100 105 110

Val Thr Gln Ser Ser Gly Lys Asn Ile Gly Ser Arg Leu Tyr Leu Leu
 115 120 125

Gln Asp Asp Thr Thr Tyr Gln Ile Phe Lys Leu Leu Gly Gln Glu Phe
 130 135 140

Thr Phe Asp Val Asp Val Ser Asn Leu Pro Cys Gly Leu Asn Gly Ala
 145 150 155 160

Leu Tyr Phe Val Ala Met Asp Ala Asp Gly Gly Leu Ser Lys Tyr Pro
 165 170 175

Gly Asn Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln
 180 185 190

Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu Gly
 195 200 205

Trp Gln Pro Ser Ala Asn Asp Pro Asn Ala Gly Val Gly Asn His Gly
 210 215 220

Ser Cys Cys Ala Glu Met Asp Val Trp Glu Ala Asn Ser Ile Ser Thr
 225 230 235 240

Ala Val Thr Pro His Pro Cys Asp Thr Pro Gly Gln Thr Met Cys Gln

	245		250		255
Gly Asp Asp Cys Gly Gly Thr Tyr Ser Ser Thr Arg Tyr Ala Gly Thr	260		265		270
Cys Asp Pro Asp Gly Cys Asp Phe Asn Pro Tyr Arg Gln Gly Asn His	275		280		285
Ser Phe Tyr Gly Pro Gly Lys Ile Val Asp Thr Ser Ser Lys Phe Thr	290		295		300
Val Val Thr Gln Phe Ile Thr Asp Asp Gly Thr Pro Ser Gly Thr Leu	305		310		315
Thr Glu Ile Lys Arg Phe Tyr Val Gln Asn Gly Lys Val Ile Pro Gln	325		330		335
Ser Glu Ser Thr Ile Ser Gly Val Thr Gly Asn Ser Ile Thr Thr Glu	340		345		350
Tyr Cys Thr Ala Gln Lys Ala Ala Phe Gly Asp Asn Thr Gly Phe Phe	355		360		365
Thr His Gly Gly Leu Gln Lys Ile Ser Gln Ala Leu Ala Gln Gly Met	370		375		380
Val Leu Val Met Ser Leu Trp Asp Asp His Ala Ala Asn Met Leu Trp	385		390		395
Leu Asp Ser Thr Tyr Pro Thr Asp Ala Asp Pro Asp Thr Pro Gly Val	405		410		415
Ala Arg Gly Thr Cys Pro Thr Thr Ser Gly Val Pro Ala Asp Val Glu	420		425		430
Ser Gln Asn Pro Asn Ser Tyr Val Ile Tyr Ser Asn Ile Lys Val Gly	435		440		445
Pro Ile Asn Ser Thr Phe Thr Ala Asn	450		455		

<210> 9
 <211> 1617
 <212> DNA
 <213> Thielavia australiensis

<220>
 <221> CDS
 <222> (1)..(1617)
 <223>

<400> 9

atg tat gcc aag ttc gcg acc ctc gcc gcc ctc gtg gct ggc gcc tcc	48
Met Tyr Ala Lys Phe Ala Thr Leu Ala Ala Leu Val Ala Gly Ala Ser	
1 5 10 15	
gcc cag gcc gtc tgc agc ctt acc gct gag acg cac cct tcc ctg acg	96
Ala Gln Ala Val Cys Ser Leu Thr Ala Glu Thr His Pro Ser Leu Thr	
20 25 30	

tgg cag aag tgc acg gcc ccc ggc agc tgc acc aac gtc gcc ggc tcc	144
Trp Gln Lys Cys Thr Ala Pro Gly Ser Cys Thr Asn Val Ala Gly Ser	
35 40 45	
atc acc atc gac gcc aac tgg cgc tgg act cac cag acc tcg tcc gcg	192
Ile Thr Ile Asp Ala Asn Trp Arg Trp Thr His Gln Thr Ser Ser Ala	
50 55 60	
acc aac tgc tac agc ggc agc aag tgg gac tcg tcc atc tgc acg acc	240
Thr Asn Cys Tyr Ser Gly Ser Lys Trp Asp Ser Ser Ile Cys Thr Thr	
65 70 75 80	
ggc acc gac tgc gcc tcc aag tgc tgc att gat ggc gcc gag tac tcg	288
Gly Thr Asp Cys Ala Ser Lys Cys Cys Ile Asp Gly Ala Glu Tyr Ser	
85 90 95	
agc acc tac ggc atc acc acc agc ggc aat gcc ctg aac ctc aag ttc	336
Ser Thr Tyr Gly Ile Thr Thr Ser Gly Asn Ala Leu Asn Leu Lys Phe	
100 105 110	
gtc acc aag ggc cag tac tcg acc aac att ggc tcg cgt acc tac ctc	384
Val Thr Lys Gly Gln Tyr Ser Thr Asn Ile Gly Ser Arg Thr Tyr Leu	
115 120 125	
atg gag tcg gac acc aag tac cag atg ttc aag ctc ctt ggc aac gag	432
Met Glu Ser Asp Thr Lys Tyr Gln Met Phe Lys Leu Leu Gly Asn Glu	
130 135 140	
ttc acc ttc gac gtc gat gtc tcc aac ctc ggc tgc ggc ctc aac ggc	480
Phe Thr Phe Asp Val Asp Val Ser Asn Leu Gly Cys Gly Leu Asn Gly	
145 150 155 160	
gcc ctg tac ttc gtc tcc atg gat gcc gac ggt ggc atg tcc aag tac	528
Ala Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Met Ser Lys Tyr	
165 170 175	
tcg ggc aac aag gcc ggt gcc aag tac ggt acc ggc tac tgc gat gct	576
Ser Gly Asn Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ala	
180 185 190	
cag tgc ccc cgc gac ctc aag ttc atc aac ggc gag gcc aac gtt gag	624
Gln Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Glu Ala Asn Val Glu	
195 200 205	
ggc tgg gag agc tcg acc aac gac gcc aac gcc ggc tcg ggc aag tac	672
Gly Trp Glu Ser Ser Thr Asn Asp Ala Asn Ala Gly Ser Gly Lys Tyr	
210 215 220	
ggc agc tgc tgc acc gag atg gac gtc tgg gag gcc aac aac atg gcg	720
Gly Ser Cys Cys Thr Glu Met Asp Val Trp Glu Ala Asn Asn Met Ala	
225 230 235 240	
act gcc ttc act cct cac cct tgc acc acc att ggc cag act cgc tgc	768
Thr Ala Phe Thr Pro His Pro Cys Thr Thr Ile Gly Gln Thr Arg Cys	
245 250 255	
gag ggc gac acc tgc ggc ggc acc tac agc tca gac cgc tac gcc ggc	816
Glu Gly Asp Thr Cys Gly Gly Thr Tyr Ser Ser Asp Arg Tyr Ala Gly	
260 265 270	
gtc tgc gac ccc gac gga tgc gac ttc aac tcg tac cgc cag ggc aac	864
Val Cys Asp Pro Asp Gly Cys Asp Phe Asn Ser Tyr Arg Gln Gly Asn	

275	280	285	
aag acc ttc tac ggc aag ggc atg acc gtc gac acc acc aag aag atc Lys Thr Phe Tyr Gly Lys Gly Met Thr Val Asp Thr Thr Lys Lys Ile 290 295 300			912
acg gtc gtc acc cag ttc ctc aag aac tcg gcc ggc gag ctc tcc gag Thr Val Val Thr Gln Phe Leu Lys Asn Ser Ala Gly Glu Leu Ser Glu 305 310 315 320			960
atc aag cgc ttc tac gcc cag gac ggc aag gtc atc ccg aac agt gag Ile Lys Arg Phe Tyr Ala Gln Asp Gly Lys Val Ile Pro Asn Ser Glu 325 330 335			1008
tct acc att gcc ggc atc ccc ggc aac tcc atc acc aag gcc tac tgc Ser Thr Ile Ala Gly Ile Pro Gly Asn Ser Ile Thr Lys Ala Tyr Cys 340 345 350			1056
gac gcc cag aag acc gtc ttc cag aac acc gac gac ttc acc gcc aag Asp Ala Gln Lys Thr Val Phe Gln Asn Thr Asp Asp Phe Thr Ala Lys 355 360 365			1104
ggc ggc ctc gtc cag atg ggc aag gcc ctc gcc ggc gac atg gtc ctc Gly Gly Leu Val Gln Met Gly Lys Ala Leu Ala Gly Asp Met Val Leu 370 375 380			1152
gtc atg tcc gtc tgg gac gac cac gcc gtc aac atg ctc tgg cta gac Val Met Ser Val Trp Asp Asp His Ala Val Asn Met Leu Trp Leu Asp 385 390 395 400			1200
tcg acc tac ccg acc gac cag gtc ggc gtt gcc ggc gct gag cgc ggc Ser Thr Tyr Pro Thr Asp Gln Val Gly Val Ala Gly Ala Glu Arg Gly 405 410 415			1248
gcc tgc ccc acc acc tcg ggc gtc ccc tcg gat gtt gag gcc aac gcc Ala Cys Pro Thr Thr Ser Gly Val Pro Ser Asp Val Glu Ala Asn Ala 420 425 430			1296
ccc aac tcc aac gtc atc ttc tcc aac atc cgc ttc ggc ccc atc ggc Pro Asn Ser Asn Val Ile Phe Ser Asn Ile Arg Phe Gly Pro Ile Gly 435 440 445			1344
tcc acc gtc cag ggc ctg ccc agc tcc ggc ggc acc tcc agc agc tcg Ser Thr Val Gln Gly Leu Pro Ser Ser Gly Gly Thr Ser Ser Ser Ser 450 455 460			1392
agc gcc gct ccc cag tcg acc agc acc aag gcc tcg acc acc acc tca Ser Ala Ala Pro Gln Ser Thr Ser Thr Lys Ala Ser Thr Thr Thr Ser 465 470 475 480			1440
gct gtc cgc acc acc tcg act gcc acc acc aag acc acc tcc tcg gct Ala Val Arg Thr Thr Ser Thr Ala Thr Thr Lys Thr Thr Ser Ser Ala 485 490 495			1488
ccc gcc cag ggc acc aac act gcc aag cat tgg cag caa tgc ggt ggt Pro Ala Gln Gly Thr Asn Thr Ala Lys His Trp Gln Gln Cys Gly Gly 500 505 510			1536
aac ggc tgg acc ggc ccg acg gtg tgc gag tct ccc tac aag tgc acc Asn Gly Trp Thr Gly Pro Thr Val Cys Glu Ser Pro Tyr Lys Cys Thr 515 520 525			1584

aag cag aac gac tgg tac tcg cag tgc ctc taa
 Lys Gln Asn Asp Trp Tyr Ser Gln Cys Leu
 530 535

1617

<210> 10
 <211> 538
 <212> PRT
 <213> Thielavia australiensis

<400> 10

Met Tyr Ala Lys Phe Ala Thr Leu Ala Ala Leu Val Ala Gly Ala Ser
 1 5 10 15

Ala Gln Ala Val Cys Ser Leu Thr Ala Glu Thr His Pro Ser Leu Thr
 20 25 30

Trp Gln Lys Cys Thr Ala Pro Gly Ser Cys Thr Asn Val Ala Gly Ser
 35 40 45

Ile Thr Ile Asp Ala Asn Trp Arg Trp Thr His Gln Thr Ser Ser Ala
 50 55 60

Thr Asn Cys Tyr Ser Gly Ser Lys Trp Asp Ser Ser Ile Cys Thr Thr
 65 70 75 80

Gly Thr Asp Cys Ala Ser Lys Cys Cys Ile Asp Gly Ala Glu Tyr Ser
 85 90 95

Ser Thr Tyr Gly Ile Thr Thr Ser Gly Asn Ala Leu Asn Leu Lys Phe
 100 105 110

Val Thr Lys Gly Gln Tyr Ser Thr Asn Ile Gly Ser Arg Thr Tyr Leu
 115 120 125

Met Glu Ser Asp Thr Lys Tyr Gln Met Phe Lys Leu Leu Gly Asn Glu
 130 135 140

Phe Thr Phe Asp Val Asp Val Ser Asn Leu Gly Cys Gly Leu Asn Gly
 145 150 155 160

Ala Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Met Ser Lys Tyr
 165 170 175

Ser Gly Asn Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ala
 180 185 190

Gln Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Glu Ala Asn Val Glu
 195 200 205

Gly Trp Glu Ser Ser Thr Asn Asp Ala Asn Ala Gly Ser Gly Lys Tyr
 210 215 220

Gly Ser Cys Cys Thr Glu Met Asp Val Trp Glu Ala Asn Asn Met Ala
 225 230 235 240

Thr Ala Phe Thr Pro His Pro Cys Thr Thr Ile Gly Gln Thr Arg Cys
 245 250 255

Glu Gly Asp Thr Cys Gly Gly Thr Tyr Ser Ser Asp Arg Tyr Ala Gly
 260 265 270

Val Cys Asp Pro Asp Gly Cys Asp Phe Asn Ser Tyr Arg Gln Gly Asn
 275 280 285
 Lys Thr Phe Tyr Gly Lys Gly Met Thr Val Asp Thr Thr Lys Lys Ile
 290 295 300
 Thr Val Val Thr Gln Phe Leu Lys Asn Ser Ala Gly Glu Leu Ser Glu
 305 310 315 320
 Ile Lys Arg Phe Tyr Ala Gln Asp Gly Lys Val Ile Pro Asn Ser Glu
 325 330 335
 Ser Thr Ile Ala Gly Ile Pro Gly Asn Ser Ile Thr Lys Ala Tyr Cys
 340 345 350
 Asp Ala Gln Lys Thr Val Phe Gln Asn Thr Asp Asp Phe Thr Ala Lys
 355 360 365
 Gly Gly Leu Val Gln Met Gly Lys Ala Leu Ala Gly Asp Met Val Leu
 370 375 380
 Val Met Ser Val Trp Asp Asp His Ala Val Asn Met Leu Trp Leu Asp
 385 390 395 400
 Ser Thr Tyr Pro Thr Asp Gln Val Gly Val Ala Gly Ala Glu Arg Gly
 405 410 415
 Ala Cys Pro Thr Thr Ser Gly Val Pro Ser Asp Val Glu Ala Asn Ala
 420 425 430
 Pro Asn Ser Asn Val Ile Phe Ser Asn Ile Arg Phe Gly Pro Ile Gly
 435 440 445
 Ser Thr Val Gln Gly Leu Pro Ser Ser Gly Gly Thr Ser Ser Ser Ser
 450 455 460
 Ser Ala Ala Pro Gln Ser Thr Ser Thr Lys Ala Ser Thr Thr Thr Ser
 465 470 475 480
 Ala Val Arg Thr Thr Ser Thr Ala Thr Thr Lys Thr Thr Ser Ser Ala
 485 490 495
 Pro Ala Gln Gly Thr Asn Thr Ala Lys His Trp Gln Gln Cys Gly Gly
 500 505 510
 Asn Gly Trp Thr Gly Pro Thr Val Cys Glu Ser Pro Tyr Lys Cys Thr
 515 520 525
 Lys Gln Asn Asp Trp Tyr Ser Gln Cys Leu
 530 535

<210> 11
 <211> 1248
 <212> DNA
 <213> *Verticillium tenerum*

<220>
 <221> CDS
 <222> (1) .. (1248)
 <223>

<400> 11

atg aag aag gct ctc atc acc agc ctc tcc ctg ctg gcc acg gcc atg	48
Met Lys Lys Ala Leu Ile Thr Ser Leu Ser Leu Leu Ala Thr Ala Met	
1 5 10 15	
ggc cag cag gcc ggt acc ctc gag acc gag acg cat ccc aag ctg acc	96
Gly Gln Gln Ala Gly Thr Leu Glu Thr Glu Thr His Pro Lys Leu Thr	
20 25 30	
tgg cag cgc tgc acc acc tcc ggc tgt acc aac gtc aac ggc gag gtc	144
Trp Gln Arg Cys Thr Thr Ser Gly Cys Thr Asn Val Asn Gly Glu Val	
35 40 45	
gtc atc gac gcc aac tgg cgt tgg gcc cac gac atc aac ggc tac gag	192
Val Ile Asp Ala Asn Trp Arg Trp Ala His Asp Ile Asn Gly Tyr Glu	
50 55 60	
aac tgc ttc gag ggc aac acc tgg acc ggc acc tgc agc ggc gcc gac	240
Asn Cys Phe Glu Gly Asn Thr Trp Thr Gly Thr Cys Ser Gly Ala Asp	
65 70 75 80	
ggc tgc gcg aag aac tgc gcc gtc gag gga gcc aac tac cag tcg acc	288
Gly Cys Ala Lys Asn Cys Ala Val Glu Gly Ala Asn Tyr Gln Ser Thr	
85 90 95	
tac ggt gtc tcg acc agc ggc aac gcc ctc tcc ctg cgc ttc gtc acc	336
Tyr Gly Val Ser Thr Ser Gly Asn Ala Leu Ser Leu Arg Phe Val Thr	
100 105 110	
gag cac gag cac ggc gtc aac acc ggt tcg cgc acg tac ctc atg gag	384
Glu His Glu His Gly Val Asn Thr Gly Ser Arg Thr Tyr Leu Met Glu	
115 120 125	
agc gcc acc aag tac cag atg ttc acc ctg atg aac aac gag ctc gcc	432
Ser Ala Thr Lys Tyr Gln Met Phe Thr Leu Met Asn Asn Glu Leu Ala	
130 135 140	
ttc gac gtc gac ctg tcc aag gtc gcc tgc ggc atg aac agc gcc ctc	480
Phe Asp Val Asp Leu Ser Lys Val Ala Cys Gly Met Asn Ser Ala Leu	
145 150 155 160	
tac ctc gtc ccc atg aag gcc gac ggc ggt ctc tcg tcc gag acc aac	528
Tyr Leu Val Pro Met Lys Ala Asp Gly Gly Leu Ser Ser Glu Thr Asn	
165 170 175	
aac aac gcc ggc gcc aag tac ggt acc ggt tac tgc gac gcc cag tgc	576
Asn Asn Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ala Gln Cys	
180 185 190	
gct cgc gat ctc aag ttc gtc aac ggc aag gcc aac atc gag ggc tgg	624
Ala Arg Asp Leu Lys Phe Val Asn Gly Lys Ala Asn Ile Glu Gly Trp	
195 200 205	
caa gcc tcc aag acc gac gag aac tct ggc gtc ggt aac atg ggc tcc	672
Gln Ala Ser Lys Thr Asp Glu Asn Ser Gly Val Gly Asn Met Gly Ser	
210 215 220	
tgc tgt gct gag att gac gtt tgg gag tcc aac cgc gag tct ttc gcc	720
Cys Cys Ala Glu Ile Asp Val Trp Glu Ser Asn Arg Glu Ser Phe Ala	
225 230 235 240	


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ttc acc cct cac gct tgc tcg cag aac gag tac cac gtc tgc acc ggc      768
Phe Thr Pro His Ala Cys Ser Gln Asn Glu Tyr His Val Cys Thr Gly
                245                      250                      255

gcc aac tgc ggc ggt acc tac tcg gac gac cgc ttc gcc ggc aag tgc      816
Ala Asn Cys Gly Gly Thr Tyr Ser Asp Asp Arg Phe Ala Gly Lys Cys
                260                      265                      270

gat gcc aac ggt tgc gac tac aac ccc ttc cgc gtg ggc aac cag aac      864
Asp Ala Asn Gly Cys Asp Tyr Asn Pro Phe Arg Val Gly Asn Gln Asn
                275                      280                      285

ttc tac ggc ccc ggc atg acc gtc aac acc aac tcc aag ttc act gtc      912
Phe Tyr Gly Pro Gly Met Thr Val Asn Thr Asn Ser Lys Phe Thr Val
                290                      295                      300

atc tct cgc ttc cgg gag aac gag gcc tac cag gtc ttc atc cag aac      960
Ile Ser Arg Phe Arg Glu Asn Glu Ala Tyr Gln Val Phe Ile Gln Asn
305                      310                      315                      320

ggc cgc acc atc gag gtc ccc cgt ccc acc ctc tcc ggc atc acc cag     1008
Gly Arg Thr Ile Glu Val Pro Arg Pro Thr Leu Ser Gly Ile Thr Gln
                325                      330                      335

ttc gag gcc aag atc acc ccc gag ttc tgc tcg acc tac ccc acc gtc     1056
Phe Glu Ala Lys Ile Thr Pro Glu Phe Cys Ser Thr Tyr Pro Thr Val
                340                      345                      350

ttc ggc gac cgc gac cgc cac ggc gag atc ggc ggc cac acc gcc ctc     1104
Phe Gly Asp Arg Asp Arg His Gly Glu Ile Gly Gly His Thr Ala Leu
                355                      360                      365

aac gcg gcc ctc cgc atg ccc atg gtc ctc gtc atg tcc atc tgg gcc     1152
Asn Ala Ala Leu Arg Met Pro Met Val Leu Val Met Ser Ile Trp Ala
                370                      375                      380

gac cac tac gcc aac atg ctc tgg ctc gac tcc atc tac ccg cca gag     1200
Asp His Tyr Ala Asn Met Leu Trp Leu Asp Ser Ile Tyr Pro Pro Glu
385                      390                      395                      400

aag agg ggc cag ccc ggc gcc cac cgc ggc cgc aga tct aga ggg tga     1248
Lys Arg Gly Gln Pro Gly Ala His Arg Gly Arg Arg Ser Arg Gly
                405                      410                      415

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<210> 12
<211> 415
<212> PRT
<213> Verticillium tenerum

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<400> 12

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Met Lys Lys Ala Leu Ile Thr Ser Leu Ser Leu Leu Ala Thr Ala Met
1                5                10                15

Gly Gln Gln Ala Gly Thr Leu Glu Thr Glu Thr His Pro Lys Leu Thr
                20                25                30

Trp Gln Arg Cys Thr Thr Ser Gly Cys Thr Asn Val Asn Gly Glu Val
35                40                45

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Val	Ile	Asp	Ala	Asn	Trp	Arg	Trp	Ala	His	Asp	Ile	Asn	Gly	Tyr	Glu	50	55	60
Asn	Cys	Phe	Glu	Gly	Asn	Thr	Trp	Thr	Gly	Thr	Cys	Ser	Gly	Ala	Asp	65	70	75
Gly	Cys	Ala	Lys	Asn	Cys	Ala	Val	Glu	Gly	Ala	Asn	Tyr	Gln	Ser	Thr	85	90	95
Tyr	Gly	Val	Ser	Thr	Ser	Gly	Asn	Ala	Leu	Ser	Leu	Arg	Phe	Val	Thr	100	105	110
Glu	His	Glu	His	Gly	Val	Asn	Thr	Gly	Ser	Arg	Thr	Tyr	Leu	Met	Glu	115	120	125
Ser	Ala	Thr	Lys	Tyr	Gln	Met	Phe	Thr	Leu	Met	Asn	Asn	Glu	Leu	Ala	130	135	140
Phe	Asp	Val	Asp	Leu	Ser	Lys	Val	Ala	Cys	Gly	Met	Asn	Ser	Ala	Leu	145	150	155
Tyr	Leu	Val	Pro	Met	Lys	Ala	Asp	Gly	Gly	Leu	Ser	Ser	Glu	Thr	Asn	165	170	175
Asn	Asn	Ala	Gly	Ala	Lys	Tyr	Gly	Thr	Gly	Tyr	Cys	Asp	Ala	Gln	Cys	180	185	190
Ala	Arg	Asp	Leu	Lys	Phe	Val	Asn	Gly	Lys	Ala	Asn	Ile	Glu	Gly	Trp	195	200	205
Gln	Ala	Ser	Lys	Thr	Asp	Glu	Asn	Ser	Gly	Val	Gly	Asn	Met	Gly	Ser	210	215	220
Cys	Cys	Ala	Glu	Ile	Asp	Val	Trp	Glu	Ser	Asn	Arg	Glu	Ser	Phe	Ala	225	230	235
Phe	Thr	Pro	His	Ala	Cys	Ser	Gln	Asn	Glu	Tyr	His	Val	Cys	Thr	Gly	245	250	255
Ala	Asn	Cys	Gly	Gly	Thr	Tyr	Ser	Asp	Asp	Arg	Phe	Ala	Gly	Lys	Cys	260	265	270
Asp	Ala	Asn	Gly	Cys	Asp	Tyr	Asn	Pro	Phe	Arg	Val	Gly	Asn	Gln	Asn	275	280	285
Phe	Tyr	Gly	Pro	Gly	Met	Thr	Val	Asn	Thr	Asn	Ser	Lys	Phe	Thr	Val	290	295	300
Ile	Ser	Arg	Phe	Arg	Glu	Asn	Glu	Ala	Tyr	Gln	Val	Phe	Ile	Gln	Asn	305	310	315
Gly	Arg	Thr	Ile	Glu	Val	Pro	Arg	Pro	Thr	Leu	Ser	Gly	Ile	Thr	Gln	325	330	335
Phe	Glu	Ala	Lys	Ile	Thr	Pro	Glu	Phe	Cys	Ser	Thr	Tyr	Pro	Thr	Val	340	345	350
Phe	Gly	Asp	Arg	Asp	Arg	His	Gly	Glu	Ile	Gly	Gly	His	Thr	Ala	Leu	355	360	365
Asn	Ala	Ala	Leu	Arg	Met	Pro	Met	Val	Leu	Val	Met	Ser	Ile	Trp	Ala	370	375	380

Asp His Tyr Ala Asn Met Leu Trp Leu Asp Ser Ile Tyr Pro Pro Glu
 385 390 395 400

Lys Arg Gly Gln Pro Gly Ala His Arg Gly Arg Arg Ser Arg Gly
 405 410 415

<210> 13
 <211> 1341
 <212> DNA
 <213> Neotermes castaneus

<220>
 <221> CDS
 <222> (1)..(1341)
 <223>

<400> 13

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atc ggc acc aaa acg gcc gag aac cac ccg aag ctg aac tgg cag aac Ile Gly Thr Lys Thr Ala Glu Asn His Pro Lys Leu Asn Trp Gln Asn 20 25 30	96
tgc gcc tcc aag ggc agc tgc tca caa gtg tcc ggc gaa gtg aca atg Cys Ala Ser Lys Gly Ser Cys Ser Gln Val Ser Gly Glu Val Thr Met 35 40 45	144
gac tcg aac tgg cgg tgg acc cac gat ggc aac ggc aag aac tgc tac Asp Ser Asn Trp Arg Trp Thr His Asp Gly Asn Gly Lys Asn Cys Tyr 50 55 60	192
gac ggc aac acc tgg atc tcc agc ctc tgc cca gac ggc aag acc tgc Asp Gly Asn Thr Trp Ile Ser Ser Leu Cys Pro Asp Gly Lys Thr Cys 65 70 75 80	240
tct gac aag tgc gtc ctc gat ggc gcc gaa tac caa gcg acc tac ggc Ser Asp Lys Cys Val Leu Asp Gly Ala Glu Tyr Gln Ala Thr Tyr Gly 85 90 95	288
atc acc tcg aac ggg acc gcg gtc acc ctc aag ttc gtc acc cac ggc Ile Thr Ser Asn Gly Thr Ala Val Thr Leu Lys Phe Val Thr His Gly 100 105 110	336
tcg tac tcg acg aac atc ggc tcc cgc ctg tat ctc ctc aag gac gaa Ser Tyr Ser Thr Asn Ile Gly Ser Arg Leu Tyr Leu Leu Lys Asp Glu 115 120 125	384
aac act tac tac atc ttc aag gtg aac aac aag gaa ttc aca ttc agc Asn Thr Tyr Tyr Ile Phe Lys Val Asn Asn Lys Glu Phe Thr Phe Ser 130 135 140	432
gtc gat gtg tcg aag ctc ccg tgc ggc ctg aac ggt gcc ctc tac ttc Val Asp Val Ser Lys Leu Pro Cys Gly Leu Asn Gly Ala Leu Tyr Phe 145 150 155 160	480
gtc tcg atg gac gcc gac ggt ggc gca gga aag tat tca ggt gcg aag Val Ser Met Asp Ala Asp Gly Gly Ala Gly Lys Tyr Ser Gly Ala Lys	528

165	170	175	
cca ggc gcg aag tac ggc ctc ggc tac tgc gat gcg caa tgc ccg agc Pro Gly Ala Lys Tyr Gly Leu Gly Tyr Cys Asp Ala Gln Cys Pro Ser			576
180	185	190	
gat ctg aag ttc atc aac ggc gaa gcg aac agc gat ggc tgg aag ccc Asp Leu Lys Phe Ile Asn Gly Glu Ala Asn Ser Asp Gly Trp Lys Pro			624
195	200	205	
cag gcg aac gac aag aat gcg gga aac ggc aaa tac gga tcg tgc tgc Gln Ala Asn Asp Lys Asn Ala Gly Asn Gly Lys Tyr Gly Ser Cys Cys			672
210	215	220	
tcg gaa atg gac gtt tgg gag gcg aac tcg cag gca aca gct tac act Ser Glu Met Asp Val Trp Glu Ala Asn Ser Gln Ala Thr Ala Tyr Thr			720
225	230	235	240
ccg cac gtc tgc aag acc acg ggc cag cag cgc tgc tcg ggc aca tcg Pro His Val Cys Lys Thr Thr Gly Gln Gln Arg Cys Ser Gly Thr Ser			768
245	250	255	
gaa tgc ggc ggc cag gat ggc gca gcg cgt ttc cag gga ctg tgc gac Glu Cys Gly Gly Gln Asp Gly Ala Ala Arg Phe Gln Gly Leu Cys Asp			816
260	265	270	
gag gac ggt tgc gac ttc aac agc tgg cgc cag ggc gac aag acg ttc Glu Asp Gly Cys Asp Phe Asn Ser Trp Arg Gln Gly Asp Lys Thr Phe			864
275	280	285	
tac ggc ccg gga ttg act gtt gac acg aag tcg ccg ttc aca gtc gtc Tyr Gly Pro Gly Leu Thr Val Asp Thr Lys Ser Pro Phe Thr Val Val			912
290	295	300	
aca caa ttc gtc gga agt ccg gtg aag gaa atc cgc agg aag tac gtc Thr Gln Phe Val Gly Ser Pro Val Lys Glu Ile Arg Arg Lys Tyr Val			960
305	310	315	320
cag aac gga aag gtg att gag aac tcg aag aac aag att tcg gga att Gln Asn Gly Lys Val Ile Glu Asn Ser Lys Asn Lys Ile Ser Gly Ile			1008
325	330	335	
gac gag acg aac gca gtg agt gat act ttc tgc gat cag caa aag aag Asp Glu Thr Asn Ala Val Ser Asp Thr Phe Cys Asp Gln Gln Lys Lys			1056
340	345	350	
gcc ttc ggt gat acg aac gat ttc aag aac aag ggc ggt ttc gct aag Ala Phe Gly Asp Thr Asn Asp Phe Lys Asn Lys Gly Gly Phe Ala Lys			1104
355	360	365	
ttg ggt cag gtg ttc gag act ggt cag gtt ctc gtg ctg tcg ctg tgg Leu Gly Gln Val Phe Glu Thr Gly Gln Val Leu Val Leu Ser Leu Trp			1152
370	375	380	
gat gac cac tcg gtt gca atg ctg tgg ttg gac tcg gcc tac cca acg Asp Asp His Ser Val Ala Met Leu Trp Leu Asp Ser Ala Tyr Pro Thr			1200
385	390	395	400
aac aag gat aag agc agc cca ggt gtt gac cgt ggg cct tgc ccg acg Asn Lys Asp Lys Ser Ser Pro Gly Val Asp Arg Gly Pro Cys Pro Thr			1248
405	410	415	

act tcc ggg aag ccg gat gat gtt gaa agc caa tct ccc gat gca acc 1296
 Thr Ser Gly Lys Pro Asp Asp Val Glu Ser Gln Ser Pro Asp Ala Thr
 420 425 430

gtc att tat ggc aac atc aag ttc ggt gca ctg gac tcc act tac 1341
 Val Ile Tyr Gly Asn Ile Lys Phe Gly Ala Leu Asp Ser Thr Tyr
 435 440 445

<210> 14
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 <212> PRT
 <213> Neotermes castaneus

<400> 14

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Ile Gly Thr Lys Thr Ala Glu Asn His Pro Lys Leu Asn Trp Gln Asn
 20 25 30

Cys Ala Ser Lys Gly Ser Cys Ser Gln Val Ser Gly Glu Val Thr Met
 35 40 45

Asp Ser Asn Trp Arg Trp Thr His Asp Gly Asn Gly Lys Asn Cys Tyr
 50 55 60

Asp Gly Asn Thr Trp Ile Ser Ser Leu Cys Pro Asp Gly Lys Thr Cys
 65 70 75 80

Ser Asp Lys Cys Val Leu Asp Gly Ala Glu Tyr Gln Ala Thr Tyr Gly
 85 90 95

Ile Thr Ser Asn Gly Thr Ala Val Thr Leu Lys Phe Val Thr His Gly
 100 105 110

Ser Tyr Ser Thr Asn Ile Gly Ser Arg Leu Tyr Leu Leu Lys Asp Glu
 115 120 125

Asn Thr Tyr Tyr Ile Phe Lys Val Asn Asn Lys Glu Phe Thr Phe Ser
 130 135 140

Val Asp Val Ser Lys Leu Pro Cys Gly Leu Asn Gly Ala Leu Tyr Phe
 145 150 155 160

Val Ser Met Asp Ala Asp Gly Gly Ala Gly Lys Tyr Ser Gly Ala Lys
 165 170 175

Pro Gly Ala Lys Tyr Gly Leu Gly Tyr Cys Asp Ala Gln Cys Pro Ser
 180 185 190

Asp Leu Lys Phe Ile Asn Gly Glu Ala Asn Ser Asp Gly Trp Lys Pro
 195 200 205

Gln Ala Asn Asp Lys Asn Ala Gly Asn Gly Lys Tyr Gly Ser Cys Cys
 210 215 220

Ser Glu Met Asp Val Trp Glu Ala Asn Ser Gln Ala Thr Ala Tyr Thr
 225 230 235 240

Pro His Val Cys Lys Thr Thr Gly Gln Gln Arg Cys Ser Gly Thr Ser

245										250					255				
Glu	Cys	Gly	Gly	Gln	Asp	Gly	Ala	Ala	Arg	Phe	Gln	Gly	Leu	Cys	Asp				
			260					265					270						
Glu	Asp	Gly	Cys	Asp	Phe	Asn	Ser	Trp	Arg	Gln	Gly	Asp	Lys	Thr	Phe				
		275					280					285							
Tyr	Gly	Pro	Gly	Leu	Thr	Val	Asp	Thr	Lys	Ser	Pro	Phe	Thr	Val	Val				
	290					295					300								
Thr	Gln	Phe	Val	Gly	Ser	Pro	Val	Lys	Glu	Ile	Arg	Arg	Lys	Tyr	Val				
305					310					315					320				
Gln	Asn	Gly	Lys	Val	Ile	Glu	Asn	Ser	Lys	Asn	Lys	Ile	Ser	Gly	Ile				
			325						330					335					
Asp	Glu	Thr	Asn	Ala	Val	Ser	Asp	Thr	Phe	Cys	Asp	Gln	Gln	Lys	Lys				
			340					345					350						
Ala	Phe	Gly	Asp	Thr	Asn	Asp	Phe	Lys	Asn	Lys	Gly	Gly	Phe	Ala	Lys				
		355					360					365							
Leu	Gly	Gln	Val	Phe	Glu	Thr	Gly	Gln	Val	Leu	Val	Leu	Ser	Leu	Trp				
	370					375					380								
Asp	Asp	His	Ser	Val	Ala	Met	Leu	Trp	Leu	Asp	Ser	Ala	Tyr	Pro	Thr				
385					390				395						400				
Asn	Lys	Asp	Lys	Ser	Ser	Pro	Gly	Val	Asp	Arg	Gly	Pro	Cys	Pro	Thr				
				405					410					415					
Thr	Ser	Gly	Lys	Pro	Asp	Asp	Val	Glu	Ser	Gln	Ser	Pro	Asp	Ala	Thr				
			420					425					430						
Val	Ile	Tyr	Gly	Asn	Ile	Lys	Phe	Gly	Ala	Leu	Asp	Ser	Thr	Tyr					
	435						440					445							

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 <211> 1359
 <212> DNA
 <213> Melanocarpus albomyces

<220>
 <221> CDS
 <222> (1)..(1359)
 <223>

<400> 15

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Met	Met	Met	Lys	Gln	Tyr	Leu	Gln	Tyr	Leu	Ala	Ala	Ala	Leu	Pro	Leu			
1				5					10					15				
gtc	ggc	ctc	gcc	gcc	ggc	cag	cgc	gct	ggt	aac	gag	acg	ccc	gag	agc			96
Val	Gly	Leu	Ala	Ala	Gly	Gln	Arg	Ala	Gly	Asn	Glu	Thr	Pro	Glu	Ser			
			20					25					30					
cac	ccc	ccg	ctc	acc	tgg	cag	agg	tgc	acg	gcc	ccg	ggc	aac	tgc	cag			144
His	Pro	Pro	Leu	Thr	Trp	Gln	Arg	Cys	Thr	Ala	Pro	Gly	Asn	Cys	Gln			
		35					40					45						

acc	gtg	aac	gcc	gag	gtc	gta	att	gac	gcc	aac	tgg	cgc	tgg	ctg	cac	192
Thr	Val	Asn	Ala	Glu	Val	Val	Ile	Asp	Ala	Asn	Trp	Arg	Trp	Leu	His	
50						55					60					
gac	gac	aac	atg	cag	aac	tgc	tac	gac	ggc	aac	cag	tgg	acc	aac	gcc	240
Asp	Asp	Asn	Met	Gln	Asn	Cys	Tyr	Asp	Gly	Asn	Gln	Trp	Thr	Asn	Ala	
65					70					75					80	
tgc	agc	acc	gcc	acc	gac	tgc	gct	gag	aag	tgc	atg	atc	gag	ggt	gcc	288
Cys	Ser	Thr	Ala	Thr	Asp	Cys	Ala	Glu	Lys	Cys	Met	Ile	Glu	Gly	Ala	
				85					90					95		
ggc	gac	tac	ctg	ggc	acc	tac	ggc	gcc	tcg	acc	agc	ggc	gac	gcc	ctg	336
Gly	Asp	Tyr	Leu	Gly	Thr	Tyr	Gly	Ala	Ser	Thr	Ser	Gly	Asp	Ala	Leu	
			100					105					110			
acg	ctc	aag	ttc	gtc	acg	aag	cac	gag	tac	ggc	acc	aac	gtc	ggc	tcg	384
Thr	Leu	Lys	Phe	Val	Thr	Lys	His	Glu	Tyr	Gly	Thr	Asn	Val	Gly	Ser	
		115					120					125				
cgc	ttc	tac	ctc	atg	aac	ggc	ccg	gac	aag	tac	cag	atg	ttc	gac	ctc	432
Arg	Phe	Tyr	Leu	Met	Asn	Gly	Pro	Asp	Lys	Tyr	Gln	Met	Phe	Asp	Leu	
	130					135					140					
ctg	ggc	aac	gag	ctt	gcc	ttt	gac	gtc	gac	ctc	tcg	acc	gtc	gag	tgc	480
Leu	Gly	Asn	Glu	Leu	Ala	Phe	Asp	Val	Asp	Leu	Ser	Thr	Val	Glu	Cys	
145					150					155					160	
ggc	atc	aac	agc	gcc	ctg	tac	ttc	gtc	gcc	atg	gag	gag	gac	ggc	ggc	528
Gly	Ile	Asn	Ser	Ala	Leu	Tyr	Phe	Val	Ala	Met	Glu	Glu	Asp	Gly	Gly	
				165					170					175		
atg	gcc	agc	tac	ccg	agc	aac	cag	gcc	ggc	gcc	cgg	tac	ggc	act	ggg	576
Met	Ala	Ser	Tyr	Pro	Ser	Asn	Gln	Ala	Gly	Ala	Arg	Tyr	Gly	Thr	Gly	
			180					185					190			
tac	tgc	gat	gcc	caa	tgc	gct	cgt	gac	ctc	aag	ttc	gtt	ggc	ggc	aag	624
Tyr	Cys	Asp	Ala	Gln	Cys	Ala	Arg	Asp	Leu	Lys	Phe	Val	Gly	Gly	Lys	
		195					200					205				
gcc	aac	att	gag	ggc	tgg	aag	ccg	tcc	acc	aac	gac	ccc	aac	gct	ggc	672
Ala	Asn	Ile	Glu	Gly	Trp	Lys	Pro	Ser	Thr	Asn	Asp	Pro	Asn	Ala	Gly	
	210					215					220					
gtc	ggc	ccg	tac	ggc	ggc	tgc	tgc	gct	gag	atc	gac	gtc	tgg	gag	tcg	720
Val	Gly	Pro	Tyr	Gly	Gly	Cys	Cys	Ala	Glu	Ile	Asp	Val	Trp	Glu	Ser	
225					230					235					240	
aac	gcc	tat	gcc	ttc	gct	ttc	acg	ccg	cac	gcg	tgc	acg	acc	aac	gag	768
Asn	Ala	Tyr	Ala	Phe	Ala	Phe	Thr	Pro	His	Ala	Cys	Thr	Thr	Asn	Glu	
				245					250					255		
tac	cac	gtc	tgc	gag	acc	acc	aac	tgc	ggt	ggc	acc	tac	tcg	gag	gac	816
Tyr	His	Val	Cys	Glu	Thr	Thr	Asn	Cys	Gly	Gly	Thr	Tyr	Ser	Glu	Asp	
			260					265					270			
cgc	ttc	gcc	ggc	aag	tgc	gac	gcc	aac	ggc	tgc	gac	tac	aac	ccc	tac	864
Arg	Phe	Ala	Gly	Lys	Cys	Asp	Ala	Asn	Gly	Cys	Asp	Tyr	Asn	Pro	Tyr	
		275					280					285				
cgc	atg	ggc	aac	ccc	gac	ttc	tac	ggc	aag	ggc	aag	acg	ctc	gac	acc	912

Arg	Met	Gly	Asn	Pro	Asp	Phe	Tyr	Gly	Lys	Gly	Lys	Thr	Leu	Asp	Thr	
290						295					300					
agc	cgc	aag	ttc	acc	gtc	gtc	tcc	cgc	ttc	gag	gag	aac	aag	ctc	tcc	960
Ser	Arg	Lys	Phe	Thr	Val	Val	Ser	Arg	Phe	Glu	Glu	Asn	Lys	Leu	Ser	
305					310					315					320	
cag	tac	ttc	atc	cag	gac	ggc	cgc	aag	atc	gag	atc	ccg	ccg	ccg	acg	1008
Gln	Tyr	Phe	Ile	Gln	Asp	Gly	Arg	Lys	Ile	Glu	Ile	Pro	Pro	Pro	Thr	
				325					330					335		
tgg	gag	ggc	atg	ccc	aac	agc	agc	gag	atc	acc	ccc	gag	ctc	tgc	tcc	1056
Trp	Glu	Gly	Met	Pro	Asn	Ser	Ser	Glu	Ile	Thr	Pro	Glu	Leu	Cys	Ser	
			340					345					350			
acc	atg	ttc	gat	gtg	ttc	aac	gac	cgc	aac	cgc	ttc	gag	gag	gtc	ggc	1104
Thr	Met	Phe	Asp	Val	Phe	Asn	Asp	Arg	Asn	Arg	Phe	Glu	Glu	Val	Gly	
		355					360					365				
ggc	ttc	gag	cag	ctg	aac	aac	gcc	ctc	cgg	gtt	ccc	atg	gtc	ctc	gtc	1152
Gly	Phe	Glu	Gln	Leu	Asn	Asn	Ala	Leu	Arg	Val	Pro	Met	Val	Leu	Val	
	370					375					380					
atg	tcc	atc	tgg	gac	gac	cac	tac	gcc	aac	atg	ctc	tgg	ctc	gac	tcc	1200
Met	Ser	Ile	Trp	Asp	Asp	His	Tyr	Ala	Asn	Met	Leu	Trp	Leu	Asp	Ser	
385					390					395					400	
atc	tac	ccg	ccc	gag	aag	gag	ggc	cag	ccc	ggc	gcc	gcc	cgt	ggc	gac	1248
Ile	Tyr	Pro	Pro	Glu	Lys	Glu	Gly	Gln	Pro	Gly	Ala	Ala	Arg	Gly	Asp	
				405				410						415		
tgc	ccc	acg	gac	tcg	ggt	gtc	ccc	gcc	gag	gtc	gag	gct	cag	ttc	ccc	1296
Cys	Pro	Thr	Asp	Ser	Gly	Val	Pro	Ala	Glu	Val	Glu	Ala	Gln	Phe	Pro	
			420					425					430			
gac	gcc	cag	gtc	gtc	tgg	tcc	aac	atc	cgc	ttc	ggc	ccc	atc	ggc	tcg	1344
Asp	Ala	Gln	Val	Val	Trp	Ser	Asn	Ile	Arg	Phe	Gly	Pro	Ile	Gly	Ser	
		435					440					445				
acc	tac	gac	ttc	taa												1359
Thr	Tyr	Asp	Phe													
	450															

<210> 16
 <211> 452
 <212> PRT
 <213> Melanocarpus albomyces

<400> 16

Met	Met	Met	Lys	Gln	Tyr	Leu	Gln	Tyr	Leu	Ala	Ala	Ala	Leu	Pro	Leu	
1				5					10					15		
Val	Gly	Leu	Ala	Ala	Gly	Gln	Arg	Ala	Gly	Asn	Glu	Thr	Pro	Glu	Ser	
			20					25					30			
His	Pro	Pro	Leu	Thr	Trp	Gln	Arg	Cys	Thr	Ala	Pro	Gly	Asn	Cys	Gln	
		35					40					45				
Thr	Val	Asn	Ala	Glu	Val	Val	Ile	Asp	Ala	Asn	Trp	Arg	Trp	Leu	His	
	50					55					60					

Asp	Asp	Asn	Met	Gln	Asn	Cys	Tyr	Asp	Gly	Asn	Gln	Trp	Thr	Asn	Ala	
65					70					75					80	
Cys	Ser	Thr	Ala	Thr	Asp	Cys	Ala	Glu	Lys	Cys	Met	Ile	Glu	Gly	Ala	
				85					90					95		
Gly	Asp	Tyr	Leu	Gly	Thr	Tyr	Gly	Ala	Ser	Thr	Ser	Gly	Asp	Ala	Leu	
			100					105					110			
Thr	Leu	Lys	Phe	Val	Thr	Lys	His	Glu	Tyr	Gly	Thr	Asn	Val	Gly	Ser	
		115					120					125				
Arg	Phe	Tyr	Leu	Met	Asn	Gly	Pro	Asp	Lys	Tyr	Gln	Met	Phe	Asp	Leu	
	130					135					140					
Leu	Gly	Asn	Glu	Leu	Ala	Phe	Asp	Val	Asp	Leu	Ser	Thr	Val	Glu	Cys	
145					150					155					160	
Gly	Ile	Asn	Ser	Ala	Leu	Tyr	Phe	Val	Ala	Met	Glu	Glu	Asp	Gly	Gly	
				165					170					175		
Met	Ala	Ser	Tyr	Pro	Ser	Asn	Gln	Ala	Gly	Ala	Arg	Tyr	Gly	Thr	Gly	
			180					185					190			
Tyr	Cys	Asp	Ala	Gln	Cys	Ala	Arg	Asp	Leu	Lys	Phe	Val	Gly	Gly	Lys	
		195					200					205				
Ala	Asn	Ile	Glu	Gly	Trp	Lys	Pro	Ser	Thr	Asn	Asp	Pro	Asn	Ala	Gly	
	210					215					220					
Val	Gly	Pro	Tyr	Gly	Gly	Cys	Cys	Ala	Glu	Ile	Asp	Val	Trp	Glu	Ser	
225					230					235					240	
Asn	Ala	Tyr	Ala	Phe	Ala	Phe	Thr	Pro	His	Ala	Cys	Thr	Thr	Asn	Glu	
				245					250					255		
Tyr	His	Val	Cys	Glu	Thr	Thr	Asn	Cys	Gly	Gly	Thr	Tyr	Ser	Glu	Asp	
			260					265					270			
Arg	Phe	Ala	Gly	Lys	Cys	Asp	Ala	Asn	Gly	Cys	Asp	Tyr	Asn	Pro	Tyr	
		275					280					285				
Arg	Met	Gly	Asn	Pro	Asp	Phe	Tyr	Gly	Lys	Gly	Lys	Thr	Leu	Asp	Thr	
	290					295					300					
Ser	Arg	Lys	Phe	Thr	Val	Val	Ser	Arg	Phe	Glu	Glu	Asn	Lys	Leu	Ser	
305					310					315					320	
Gln	Tyr	Phe	Ile	Gln	Asp	Gly	Arg	Lys	Ile	Glu	Ile	Pro	Pro	Pro	Thr	
				325					330					335		
Trp	Glu	Gly	Met	Pro	Asn	Ser	Ser	Glu	Ile	Thr	Pro	Glu	Leu	Cys	Ser	
			340					345					350			
Thr	Met	Phe	Asp	Val	Phe	Asn	Asp	Arg	Asn	Arg	Phe	Glu	Glu	Val	Gly	
		355					360					365				
Gly	Phe	Glu	Gln	Leu	Asn	Asn	Ala	Leu	Arg	Val	Pro	Met	Val	Leu	Val	
	370					375					380					
Met	Ser	Ile	Trp	Asp	Asp	His	Tyr	Ala	Asn	Met	Leu	Trp	Leu	Asp	Ser	

```
<210> 19
<211> 199
<212> DNA
<213> Cladorrhinum foecundissimum
```


<220>
 <221> misc_feature
 <222> (1)..(199)
 <223> Partial CBH1 encoding sequence

<400> 19

```
tacataaacg gtatcggcaa cgttgagggt tggtcctcct ctaccaacga tcccaacgct      60
ggtgtcggta accrcggtac ttgctgctcc gagaatggat atctgggagg ccaacaagat      120
ctcgaccgcc tacactcccc acccctgcac caccatcgac cagcacatgt gcgagggcaa      180
ctcgtgcggc ggaacctac                                          199
```

<210> 20
 <211> 191
 <212> DNA
 <213> Diplodia gossypina

<220>
 <221> misc_feature
 <222> (1)..(191)
 <223> Partial CBH1 encoding sequence

<400> 20

```
gttgatccga cggcaaggcc caacgtcgag ggctgggtcc cgtccgagaa cgactccaac      60
gctgggtgtcg gcaaccttgg ctcttgctgt gctgagatgg atatctggga ggccaactcc      120
atctcgaccg cctacacccc ccacagctgc aagacggtcg cccagcactc ttgcactggc      180
gacgactgcg g                                          191
```

<210> 21
 <211> 232
 <212> DNA
 <213> Myceliophthora thermophila

<220>
 <221> misc_feature
 <222> (1)..(232)
 <223> Partial CBH1 encoding sequence

<400> 21

```
gggtactgcg acgcccattg cgcacgcgac ctcaagttcg tcggcgggcaa gggcaacatc      60
gagggctgga agccgtccac caacgatgcc aatgccggtg tcggtcctta tggcgggtgc      120
tgcgctgaga tcgacgtctg ggagtcgaac aagtatgctt tcgctttcac cccgcacggt      180
tgcgagaacc ctaaatacca cgtctgcgag accaccaact gcggcggcac ct          232
```

<210> 22
 <211> 467
 <212> DNA

<213> Rhizomucor pusillus

<220>

<221> misc_feature

<222> (1)..(467)

<223> Partial CBH1 encoding sequence

<400> 22

tccttcgcct ttacccccca cgcttgctcg cagnaacgag taccacgtct gcaccaccaa	60
caactgcggc ggcacctact cggacgaccg ctctgcgggc aagtgcgacg ccaacgggtg	120
cgactacaac ccgttccgcc tgggcaacca ggacttctac ggcccgggca tgaccgtcga	180
caccaactcc aagttcaccg tcatctcccg ctctcaggag aacgaggcct accagggtctt	240
catgcagggc ggccggacca tcgagggtccc ggccccgcag ctgtccgggc tcaccagtt	300
cgacgccaag atcacccccg agttctgcga cacctaccg accgtcttcg acgaccgcaa	360
ccgccacggc gagatcggcg gccacaccgc cctcaacgcc gccctgcgca tgcccatggt	420
cctcgtcatg tccatctggg ctgaccacta cgccagctgc tagtgtc	467

<210> 23

<211> 534

<212> DNA

<213> Meripilus giganteus

<220>

<221> misc_feature

<222> (1)..(534)

<223> Partial CBH1 encoding sequence

<400> 23

gggagggctc cccgaacgac ccgaacgcgg gaagcggcca gtacggaacg tgctgcaacg	60
agatggacat ctgggaggcg aaccagaacg gcgcggcggt cagcgcgcac gtctgctccg	120
tcgacggcca gacgcgctgc gagggcacgg actgcggcga cggcgacgag cggtagcagc	180
gcatctgcga caaggacggc tgcgacttca actcgtaccg catgggcgac cagtccttcc	240
tcggcctcgg caagaccgtc gacacctcga agaagttcac cgtcgtcacc cagttcctca	300
ccgcggacaa cacgacgtcc ggccagctca cggagatccg ccggctgtac gtgcaggacg	360
gcaaggatcat cgcgaactcg aagacgaaca tccccggcct cgactcgttc gactccatca	420
ccgacgactt ctgcaacgcg cagaaggagg tcttcggcga caccaactcg ttcgagaagc	480
tcggcggcct cgcggagatg ggcaaggcct tccagaaggg catggtcctc gtca	534

<210> 24

<211> 563

<212> DNA

<213> Exidia glandulosa

<220>
 <221> misc_feature
 <222> (1)..(563)
 <223> Partial CBH1 encoding sequence

<400> 24

```
gccacgtcga gggctggact ccttcmccaa cgatgccaac gccggcattg gcacccacgg      60
ctcctgctgt tcggagatgg acatctggga ggctaacaat gttgccgctg cgtacacccc     120
ccatccttgc acaactatcg gccagtcgat ctgctcgggc gattcttgcg gaggaaccta     180
cagctctgac cgttacgccg gtgtctgcga tccagacggg tgcgatttca acagctaccg     240
catgggacgac acgggcttct acggcaaggg cctgacagtc gacacgagct ccaagttcac     300
cgtcgtcacc cagttcctca ccggctccga cggcaacctt tccgagatca agcgcttcta     360
cgtccagaac ggcaaggtca ttcccaactc gcagtccaag attgccggcg tcagcggcaa     420
ctccatcacc accgacttct gctccgcccga gaagaccgcc ttcggcgaca ccaacgtctt     480
cgcgcaaaaag ggaggtactc gccgggatgg gcgccgcctt caaggccggc atggtcctcg     540
tcatgtccat ctgggacgac cac                                             563
```

<210> 25
 <211> 218
 <212> DNA
 <213> Xylaria hypoxylon

<220>
 <221> misc_feature
 <222> (1)..(218)
 <223> Partial CBH1 encoding sequence

<400> 25

```
gacgctcagt gtgcccgtga cttgaagtgc gtcgggtggca agggcaacgt tgagggatgg      60
gagccatcca ccaacgacga caacgccggg gttggccctt acggwgcctg ctgtgccgaa     120
atgatgtst gggagtccaa ctstcactct ttcgctttca cccctcacc wtgcaccacc     180
aacgaatacc acgtctgtga gcaggacgag tgtggcgg                                218
```

<210> 26
 <211> 492
 <212> DNA
 <213> Acremonium sp.

<220>

<221> misc_feature
 <222> (1)..(492)
 <223> Partial CBH1 encoding sequence

<400> 26

```

gggacgggggt actgcgacgc ccaatgcgcc cgtgatctca agttcgtcgg cggcaaggcc      60
aacattgagg gctggaggcc gtccaccaac gacgcgaacg ccggcgtcgg cccgatgggc      120
ggctgctgcg cggaaatcga tgtctgggag tccaacgccc acgcttttgc cttcacgccg      180
cacgcgtgcg agaacaacaa ctaccacatc tgcgagacct ccaactgcgg cggtagctac      240
tccgacgacc gcttcgccgg cctctgcgac gccaacggct gcgactacaa cccgtaccgc      300
atgggcaacc ccgacttcta cggcaagggc aagactcttg acacctcgcg gaagttcacc      360
gtcgtcaccg gctttcagga gaacgacctc tcgcagtact tcgtccagga cggcccgaag      420
atcgagatcc cgcccccgac ctgggacggc ctcccgaaga gcagcacata cgccgagctg      480
tgcgcgaccc ag                                          492

```

```

<210> 27
<211> 481
<212> DNA
<213> Acremonium sp.

```

```

<220>
<221> misc_feature
<222> (1)..(481)
<223> Partial CBH1 encoding sequence

```

```

<400> 27

```

```

ggctccgttt actcctaccc ttgcacggaa atcggccaga gccgctgcga gggcgacagc      60
tgccggcggtta cctacagcac cgaccgctac gctggcgtct gcgaccccga tggatgcgac      120
ttcaactcgt accgccaggg caacaagacc ttctatggca agggcatgac cgtcgacacc      180
accaagaaga ttaccgtcgt caccagttc ctcaccgact cgtccggcaa cctgtccgag      240
atcaagcgct tctacgcccga gaacggcgtc gtcaccccca actccgagtc caccattgct      300
ggcgtccctg gcaactcgat caccaggac tactgcgaca agcagaagac cgcctttggt      360
gacaacaacg acttcgacaa gaaggggtggt ctgcgccaga tgggtaaggc cctggcccaa      420
cccatgggtcc tcgtcatgtc cgtctgggat gaccatgccg tcaacatgct ctgcttcgaa      480
a                                          481

```

```

<210> 28
<211> 463
<212> DNA
<213> Chaetomium sp.

```

```

<220>
<221> misc_feature
<222> (1)..(463)
<223> Partial CBH1 encoding sequence

```

```

<400> 28

```

```

ctccccgtct tcacgccgca cgcgtgcaag aacatcaagt accacgtctg cgagacgtcg      60
ggatgcggcg gcacctactc ggaggaccgc ttgcgggcg actgcgacgc caacggttgc      120
gactacaacc cctaccgcat gggcaacacc gacttctacg gcaagggcat gacggtcgac      180
accagcaaga agttcacctg cgtgacccaa ttccaggaga acaagctcac ccagttcttc      240
gtccagaacg gcaagaagat cgagatccct ggccccaagt gggacggcat tgagggcgac      300
agcgccgcca tcacgccccca gctgtgcact tccatgttca aggccttcga cgaccgcat      360
cgcttctcgg aggtcggcgg cttcaccag atcaaccagg ccctctcggg gcccatgggtg      420
ctcgtcatgt ccatctggga cgaccactac gccaacatgc ttg                        463

```

```

<210> 29
<211> 513
<212> DNA
<213> Chaetomidium pingtungium

<220>
<221> misc_feature
<222> (1)..(513)
<223> Partial CBH1 encoding sequence

<400> 29

```

```

gaagggtggc agccctcctc caacgatgcc aatgcgggta ccggcaacca cgggtcctgc      60
tgcgcggaga tggatatctg ggaggccaac agcatctcca cggccttcac ccccatccg      120
tgcgacacgc ccggccaggt gatgtgcacc ggtgatgcct gcggtggcac ctacagctcc      180
gaccgctacg gcggcacctg cgaccccgac ggatgtgatt tcaactcctt ccgccagggc      240
aacaagacct tctacggccc tggcatgacc gtcgacacca agagcaagtt taccgtcgtc      300
accagttca tcaccgacga cggcacctcc agcggcaccc tcaaggagat caagcgcttc      360
tacgtgcaga acggcaaggt gatccccaac tcggagtcga cctggaccgg cgtcagcggc      420
aactccatca ccaccgagta ctgcaccgcc cagaagagcc tgttccagga ccagaacgtc      480
ttcgaaaagc acggtggcct cgagggcatg ggt                        513

```

```

<210> 30
<211> 579
<212> DNA
<213> Myceliophthora thermophila

```

```

<220>
<221> misc_feature
<222> (1)..(579)
<223> Partial CBH1 encoding sequence

<400> 30

```

```

gagatggata ttgaggaggc caacaacatg gccgccgcct tactcccca cccttgacc      60

```



```

gtgatcggcc agtcgcgctg cgagggcgac tcgtgcggcg gtacctacag caccgaccgc      120
tatgccggca tctgcgaccc cgacggatgc gacttcaact cgtaccgcca gggcaacaag      180
accttctacg gcaagggcat gacggtcgac acgaccaaga agatcacggc cgtcaccacg      240
ttcctcaaga actcggccgg cgagctctcc gagatcaagc ggttctacgt ccagaacggc      300
aagggtcatcc ccaactccga gtccaccatc ccgggcgctcg agggcaactc cattaccacg      360
gactgggtgcg accgccagaa ggccgctttc ggcgacgtga ccgactttca ggacaagggc      420
ggcatgggtcc agatggggcaa ggccctcgcg ggcccaatgg tcctcgatcat gtccatctgg      480
gacgaccacg ccgtcaacat gctctggctc gaaatcacta gtgcggccgc tgcaggtcga      540
ccatatggga gagctccacg cgttggatgc atagcttga                               579

```

```

<210> 31
<211> 514
<212> DNA
<213> Myceliophthora hinnulea

<220>
<221> misc_feature
<222> (1)..(514)
<223> Partial CBH1 encoding sequence

<400> 31

```

```

cgtgagggct gggagagctc gaccaacgat gccaacgccg gcacgggcag gtacggcagc      60
tgctgctccg agatggacgt ctgggaggcc aacaacatgg ccaccgcctt cccccccat      120
ccttgcacca tcatcggcca gtcgcgctgc gagggcgaga cgtgcggcgg cacctacagc      180
tcggaccgct acgccggcgt ctgcgacccc gacggctgcg acttcaactc gtaccgccag      240
ggcaacaaga ctttctacgg caagggcatg acggtcgaca cgaccaagaa gctcacggtc      300
gtcacgcagt tcctcaagaa ctcgccggcg gagctgtccg agatcaagcg gttctacgtc      360
caggacggca aggtgatccc caactccgag tccaccatcc ccggcgtcga gggcaactcg      420
atcacgcagg actggtgcga ccgccagaag gccgccttcg gcgacgtcac cgacttccag      480
gacaagggcg gcatgggtcca gatggcaagg cgct                               514

```

```

<210> 32
<211> 477
<212> DNA
<213> Sporotrichum pruinosum

<220>
<221> misc_feature
<222> (1)..(477)
<223> Partial CBH1 encoding sequence

<400> 32

```

```

cacccttgcc gcaccacgaa cgacggtggc taccaacgct gccaaggacg tgactgcaac      60
cagcctcggtt atgaggggtct ttgcgatacct gacggttgcg actacaaccc tttccgtatg    120
ggtaaccgcg aattctacgg ccctggaaag accgtcgaca ccaacaggaa gttcactgtt      180
gtgacccaat tcattaccga caacaactct gacactggta ccctcgtcga catccgccgc      240
ctctacgtcc aagacggccg tgtcattgcc aaccctccca ccaacttccc cggctctcatg     300
cccgccacg actccatcac ttagcaattc tgtgacgacg ccaagcgagc attcgaggac      360
aacgacagct ttggcaggaa cggtgggtctt gctcacatgg gtcgctccct tgccaagggc     420
catgtcctcg ccctttccat ttggaatgat cacactgcca acatgctctg gctcgaa        477

```

```

<210> 33
<211> 500
<212> DNA
<213> Thielavia cf. microspora

```

```

<220>
<221> misc_feature
<222> (1)..(500)
<223> Partial CBH1 encoding sequence

```

```

<400> 33

```

```

gagatagatg tctgggagtc caactcgcac tcgtttgcct tcacgccgca cgcgtgcaag      60
aacaacaagt accacgtctg ccagacgacc gggtgcgggc gcacctactc ggaggaccgc     120
ttcgccggcg actgcgacgc caacggctgc gactacaacc cctaccgcat gggcaacacc      180
gacttttacg gcaagggcaa gacggtcgac acgagcaaga agtttaccat ggtgacccag      240
ttccaaaaga acaagctcgt ccagttcttt gtccaggacg gcaagaagat cgacatcccc      300
ggccccaagt gggacggcct gccgcagggc agcgccgcca tcaccccgga gctgtgcacc      360
ttcatgttca aggccttcaa cgaccgacgac cgcttctcag aggttggcgg cttcgaccag      420
atcaacacgg ccctctcggg gccaatgggtg ctcgatcatgt ccatctggga tgatcactac     480
gccaacatgc tctggcttga                                                500

```

```

<210> 34
<211> 470
<212> DNA
<213> Scytalidium sp.

```

```

<220>
<221> misc_feature
<222> (1)..(470)
<223> Partial CBH1 encoding sequence

```

```

<400> 34

```

```

cgtnnggcc gcgtcgcatg ctcccgcccg catggcccg cggatttcca gccagagcat      60

```

gttggagtgg tggatcatccc agatggacat gacaaggacc atgggaatgg tgagggcctc 120
gttcagagca tcgaagccac cgggtctcggc gaagcgggtg cggatcatcga agacgcggaa 180
ctgagcatcg cagagctcag ggggtgatgtc ggcgctgttc gggaggccgg gccaggtcgg 240
agggggcacc tcgatcttgc ggccgtcctg gacgaagaac tgagagagcc tgttacgctc 300
gaagcgggag acaacgggtga acttgcggtt ggtgtcgacg gtcttgcctt tgccatagaa 360
gtccttggtg cccatgcggt aggggttgta gtcgcagccg ttggcatcgc agtagccggc 420
gaagcgggtca tccgagtagg taccaccgca gttgttggtc tccagatgtg 470

<210> 35
<211> 491
<212> DNA
<213> *Scytalidium* sp.

<220>
<221> misc_feature
<222> (1)..(491)
<223> Partial CBH1 encoding sequence

<400> 35

gaaatcgacg tctgggagtc gaacgcctat gcctatgcct taccgccac gcttgccgca 60
gccagaaccg ctaccacgtc tgcgagacca acaactgcgg tggtagctac tcggatgacc 120
gcttcgccgg ttactgcgat gccaacggct gcgactacaa cccgtaccgc atgggcaaca 180
gggacttcta cggcaagggc ctgcaggctg acaccagccg gaagttcacc gtcgtgagcc 240
gcttcgagcg caacaagctc acccagttct tcgttcagga cggccgcaag atcgagcccc 300
ctgcgccgac ctgggacggc atcccgaaga gcgccgacat ccccccgag ttctgcagcg 360
cccagttcaa ggtcttcgac gaccgtgacc gcttcgcgga gactggcggc ttcgatgccc 420
tgaacgatgc tctcagcatt cccatgggtc ttgtcatgtc catctgggat taccactact 480
ccaacataat c 491

<210> 36
<211> 221
<212> DNA
<213> *Trichophaea saccata*

<220>
<221> misc_feature
<222> (1)..(221)
<223> Partial CBH1 encoding sequence

<400> 36

tgcgactccc agtgtccccg cgatctcaag ttcataaatg gacagggcaa cggtgaaggc 60
tggaagccat cctcaaatga tgccaacgca ggcgtcgggg gacacgggtc ctgctgcgca 120

gagatggatg tttgggaggc caattccatc tccgcggccg taacaccgca ctcgtgctcc 180
acaaccagcc agacgatgtg caacggcgac tcctgcggcg g 221

<210> 37
<211> 1365
<212> DNA
<213> *Diplodia gossypina*

<220>
<221> CDS
<222> (1)..(1365)
<223>

<400> 37

atg ctt acc cag gca gtt ctc gct act ctc gcc acc ctg gcc gcc agc	48
Met Leu Thr Gln Ala Val Leu Ala Thr Leu Ala Thr Leu Ala Ala Ser	
1 5 10 15	
cag cag gtc ggc acc cag aag gag gag gtc cac ccc tcc atg acc tgg	96
Gln Gln Val Gly Thr Gln Lys Glu Glu Val His Pro Ser Met Thr Trp	
20 25 30	
cag act tgc acc agc agc ggc tgc acc acc aac cag ggc tcc atc gtc	144
Gln Thr Cys Thr Ser Ser Gly Cys Thr Thr Asn Gln Gly Ser Ile Val	
35 40 45	
gtt gac gcc aac tgg cgc tgg gtc cac aac acc gag ggc tac acc aac	192
Val Asp Ala Asn Trp Arg Trp Val His Asn Thr Glu Gly Tyr Thr Asn	
50 55 60	
tgc tac acg ggc aac acc tgg aac gcc gac tac tgc acc gac aac acc	240
Cys Tyr Thr Gly Asn Thr Trp Asn Ala Asp Tyr Cys Thr Asp Asn Thr	
65 70 75 80	
gag tgc gcc tcc aac tgc gcc ctc gac ggc gcc gac tac tct ggc acc	288
Glu Cys Ala Ser Asn Cys Ala Leu Asp Gly Ala Asp Tyr Ser Gly Thr	
85 90 95	
tac ggc gct acc acc tcc ggc gac tcg ctg cgc ctg aac ttc atc acc	336
Tyr Gly Ala Thr Thr Ser Gly Asp Ser Leu Arg Leu Asn Phe Ile Thr	
100 105 110	
aac ggc cag cag aag aac att ggc tcc cgc atg tac ctc atg cag gat	384
Asn Gly Gln Gln Lys Asn Ile Gly Ser Arg Met Tyr Leu Met Gln Asp	
115 120 125	
gac gag acc tac gcc gtc cac aag ctc ctc aac aag gag ttc acc ttc	432
Asp Glu Thr Tyr Ala Val His Lys Leu Leu Asn Lys Glu Phe Thr Phe	
130 135 140	
gac gtc gac acc tcc aag ctg cct tgc ggc ctc aac ggt gcc gtc tac	480
Asp Val Asp Thr Ser Lys Leu Pro Cys Gly Leu Asn Gly Ala Val Tyr	
145 150 155 160	
ttc gtc tcc atg gac gct gac ggt ggc atg gcc aag ttc ccc gac aac	528
Phe Val Ser Met Asp Ala Asp Gly Gly Met Ala Lys Phe Pro Asp Asn	
165 170 175	

aag gcc ggc gcc aag tac ggt acc ggt tac tgc gac tcg cag tgc ccc Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys Pro 180 185 190	576
cgt gac ctc aag ttc atc gac ggc aag gcc aac gtc gag ggc tgg gtc Arg Asp Leu Lys Phe Ile Asp Gly Lys Ala Asn Val Glu Gly Trp Val 195 200 205	624
ccg tcc gag aac gac tcc aac gct ggt gtc ggc aac ctt ggc tct tgc Pro Ser Glu Asn Asp Ser Asn Ala Gly Val Gly Asn Leu Gly Ser Cys 210 215 220	672
tgt gct gag atg gat atc tgg gag gcc aac tcc atc tcg acc gcc tac Cys Ala Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Thr Ala Tyr 225 230 235 240	720
acc ccc cac agc tgc aag acg gtc gcc cag cac tct tgc act ggc gac Thr Pro His Ser Cys Lys Thr Val Ala Gln His Ser Cys Thr Gly Asp 245 250 255	768
gac tgc ggt ggc acc tac tcc gcg acc cgc tac gcc ggc gac tgc gac Asp Cys Gly Gly Thr Tyr Ser Ala Thr Arg Tyr Ala Gly Asp Cys Asp 260 265 270	816
ccc gac gga tgc gac ttc aac tcg tac cgc cag ggc gtc aag gac ttc Pro Asp Gly Cys Asp Phe Asn Ser Tyr Arg Gln Gly Val Lys Asp Phe 275 280 285	864
tac ggg ccc ggc atg acc gtc gac agc aac tcg gtc gtc acc gtc gtc Tyr Gly Pro Gly Met Thr Val Asp Ser Asn Ser Val Val Thr Val Val 290 295 300	912
acg cag ttc atc acc aac gac ggc acc gcg tcc ggc acc ctc tcc gag Thr Gln Phe Ile Thr Asn Asp Gly Thr Ala Ser Gly Thr Leu Ser Glu 305 310 315 320	960
atc aag cgc ttc tac gtc cag aac ggc aag gtt atc ccc aac tcc gag Ile Lys Arg Phe Tyr Val Gln Asn Gly Lys Val Ile Pro Asn Ser Glu 325 330 335	1008
tcc acc atc gcc ggc gtc agc ggc aac agc atc acc tcc gcg tac tgc Ser Thr Ile Ala Gly Val Ser Gly Asn Ser Ile Thr Ser Ala Tyr Cys 340 345 350	1056
gac gcg cag aag gag gtc ttc ggc gac aac acg tcg ttc cag gac cag Asp Ala Gln Lys Glu Val Phe Gly Asp Asn Thr Ser Phe Gln Asp Gln 355 360 365	1104
ggc ggc ttg gcc agc atg agc cag gcc ctc aac gcc ggc atg gtc ctc Gly Gly Leu Ala Ser Met Ser Gln Ala Leu Asn Ala Gly Met Val Leu 370 375 380	1152
gtc atg tcc atc tgg gac gac cac cac agc aac atg ctc tgg ctc gac Val Met Ser Ile Trp Asp Asp His His Ser Asn Met Leu Trp Leu Asp 385 390 395 400	1200
tcc gac tac ccc gtc gac gcc gac ccg agc cag ccc ggc atc tcc cgc Ser Asp Tyr Pro Val Asp Ala Asp Pro Ser Gln Pro Gly Ile Ser Arg 405 410 415	1248
ggt act tgc ccc acc acc tct ggt gtc ccc agc gag gtt gag gag agc Gly Thr Cys Pro Thr Thr Ser Gly Val Pro Ser Glu Val Glu Glu Ser 1296	

420 425 430
gcc gct agc gcc tac gtc gtc tac tcg aac att aag gtt ggt gac ctt 1344
Ala Ala Ser Ala Tyr Val Val Tyr Ser Asn Ile Lys Val Gly Asp Leu
435 440 445

aac agc act ttc tct gct tag 1365
Asn Ser Thr Phe Ser Ala
450

<210> 38
<211> 454
<212> PRT
<213> *Diplodia gossypina*

<400> 38

Met Leu Thr Gln Ala Val Leu Ala Thr Leu Ala Thr Leu Ala Ala Ser
1 5 10 15

Gln Gln Val Gly Thr Gln Lys Glu Glu Val His Pro Ser Met Thr Trp
20 25 30

Gln Thr Cys Thr Ser Ser Gly Cys Thr Thr Asn Gln Gly Ser Ile Val
35 40 45

Val Asp Ala Asn Trp Arg Trp Val His Asn Thr Glu Gly Tyr Thr Asn
50 55 60

Cys Tyr Thr Gly Asn Thr Trp Asn Ala Asp Tyr Cys Thr Asp Asn Thr
65 70 75 80

Glu Cys Ala Ser Asn Cys Ala Leu Asp Gly Ala Asp Tyr Ser Gly Thr
85 90 95

Tyr Gly Ala Thr Thr Ser Gly Asp Ser Leu Arg Leu Asn Phe Ile Thr
100 105 110

Asn Gly Gln Gln Lys Asn Ile Gly Ser Arg Met Tyr Leu Met Gln Asp
115 120 125

Asp Glu Thr Tyr Ala Val His Lys Leu Leu Asn Lys Glu Phe Thr Phe
130 135 140

Asp Val Asp Thr Ser Lys Leu Pro Cys Gly Leu Asn Gly Ala Val Tyr
145 150 155 160

Phe Val Ser Met Asp Ala Asp Gly Gly Met Ala Lys Phe Pro Asp Asn
165 170 175

Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys Pro
180 185 190

Arg Asp Leu Lys Phe Ile Asp Gly Lys Ala Asn Val Glu Gly Trp Val
195 200 205

Pro Ser Glu Asn Asp Ser Asn Ala Gly Val Gly Asn Leu Gly Ser Cys
210 215 220

Cys Ala Glu Met Asp Ile Trp Glu Ala Asn Ser Ile Ser Thr Ala Tyr
225 230 235 240

Thr Pro His Ser Cys Lys Thr Val Ala Gln His Ser Cys Thr Gly Asp
 245 250 255
 Asp Cys Gly Gly Thr Tyr Ser Ala Thr Arg Tyr Ala Gly Asp Cys Asp
 260 265 270
 Pro Asp Gly Cys Asp Phe Asn Ser Tyr Arg Gln Gly Val Lys Asp Phe
 275 280 285
 Tyr Gly Pro Gly Met Thr Val Asp Ser Asn Ser Val Val Thr Val Val
 290 295 300
 Thr Gln Phe Ile Thr Asn Asp Gly Thr Ala Ser Gly Thr Leu Ser Glu
 305 310 315 320
 Ile Lys Arg Phe Tyr Val Gln Asn Gly Lys Val Ile Pro Asn Ser Glu
 325 330 335
 Ser Thr Ile Ala Gly Val Ser Gly Asn Ser Ile Thr Ser Ala Tyr Cys
 340 345 350
 Asp Ala Gln Lys Glu Val Phe Gly Asp Asn Thr Ser Phe Gln Asp Gln
 355 360 365
 Gly Gly Leu Ala Ser Met Ser Gln Ala Leu Asn Ala Gly Met Val Leu
 370 375 380
 Val Met Ser Ile Trp Asp Asp His His Ser Asn Met Leu Trp Leu Asp
 385 390 395 400
 Ser Asp Tyr Pro Val Asp Ala Asp Pro Ser Gln Pro Gly Ile Ser Arg
 405 410 415
 Gly Thr Cys Pro Thr Thr Ser Gly Val Pro Ser Glu Val Glu Glu Ser
 420 425 430
 Ala Ala Ser Ala Tyr Val Val Tyr Ser Asn Ile Lys Val Gly Asp Leu
 435 440 445
 Asn Ser Thr Phe Ser Ala
 450

<210> 39
 <211> 1377
 <212> DNA
 <213> Trichophaea saccata

<220>
 <221> CDS
 <222> (1)..(1377)
 <223>

<400> 39

atg caa cgc ctt ctc gtt ctt ctc acc tcc ctt ctc gct ttc acc tat 48
 Met Gln Arg Leu Leu Val Leu Leu Thr Ser Leu Leu Ala Phe Thr Tyr
 1 5 10 15
 ggc caa caa gtt ggc act caa cag gcc gaa gtc cac ccc tcg atg acc 96
 Gly Gln Gln Val Gly Thr Gln Gln Ala Glu Val His Pro Ser Met Thr

20				25				30								
tgg	cag	cag	tgt	aca	aag	tcc	ggc	ggc	tgc	acc	acg	aag	aac	ggc	aaa	144
Trp	Gln	Gln	Cys	Thr	Lys	Ser	Gly	Gly	Cys	Thr	Thr	Lys	Asn	Gly	Lys	
		35					40					45				
gtc	gtg	atc	gat	gcc	aac	tgg	cgt	tgg	gta	cac	aat	gtc	ggc	ggc	tac	192
Val	Val	Ile	Asp	Ala	Asn	Trp	Arg	Trp	Val	His	Asn	Val	Gly	Gly	Tyr	
	50					55					60					
acc	aat	tgc	tac	act	ggc	aac	acc	tgg	gac	agt	tcg	ctt	tgt	ccc	gac	240
Thr	Asn	Cys	Tyr	Thr	Gly	Asn	Thr	Trp	Asp	Ser	Ser	Leu	Cys	Pro	Asp	
65					70				75					80		
gat	gtc	acc	tgc	gcg	aag	aat	tgc	gct	ctt	gat	ggc	gcg	gac	tac	tct	288
Asp	Val	Thr	Cys	Ala	Lys	Asn	Cys	Ala	Leu	Asp	Gly	Ala	Asp	Tyr	Ser	
				85				90						95		
ggc	act	tat	gga	gtt	act	gcg	ggc	ggg	aat	tcg	ttg	aag	ctc	acc	ttc	336
Gly	Thr	Tyr	Gly	Val	Thr	Ala	Gly	Gly	Asn	Ser	Leu	Lys	Leu	Thr	Phe	
			100				105						110			
gtc	act	aag	ggt	caa	tac	tct	act	aat	gtg	ggc	tcg	cga	ttg	tat	atg	384
Val	Thr	Lys	Gly	Gln	Tyr	Ser	Thr	Asn	Val	Gly	Ser	Arg	Leu	Tyr	Met	
		115					120					125				
ctc	gcc	gac	gac	agc	aca	tac	cag	atg	tat	aat	ctg	ctg	aac	cag	gag	432
Leu	Ala	Asp	Asp	Ser	Thr	Tyr	Gln	Met	Tyr	Asn	Leu	Leu	Asn	Gln	Glu	
	130					135					140					
ttt	acg	ttc	gac	gtt	gat	gtt	tct	aat	ctt	cct	tgt	ggg	ctt	aac	ggg	480
Phe	Thr	Phe	Asp	Val	Asp	Val	Ser	Asn	Leu	Pro	Cys	Gly	Leu	Asn	Gly	
145					150				155					160		
gct	ctg	tat	ttc	gtc	tcg	atg	gat	aag	gat	ggt	ggg	atg	tcg	aag	tac	528
Ala	Leu	Tyr	Phe	Val	Ser	Met	Asp	Lys	Asp	Gly	Gly	Met	Ser	Lys	Tyr	
				165				170					175			
tct	ggg	aac	aag	gct	ggt	gcc	aag	tat	gga	act	ggg	tac	tgc	gac	tcc	576
Ser	Gly	Asn	Lys	Ala	Gly	Ala	Lys	Tyr	Gly	Thr	Gly	Tyr	Cys	Asp	Ser	
			180				185						190			
cag	tgt	ccc	cgc	gat	ctc	aag	ttc	atc	aat	gga	cag	ggc	aac	gtt	gaa	624
Gln	Cys	Pro	Arg	Asp	Leu	Lys	Phe	Ile	Asn	Gly	Gln	Gly	Asn	Val	Glu	
		195					200					205				
ggc	tgg	aag	cca	tcc	tca	aat	gat	gcc	aac	gca	ggc	gtc	ggg	gga	cac	672
Gly	Trp	Lys	Pro	Ser	Ser	Asn	Asp	Ala	Asn	Ala	Gly	Val	Gly	Gly	His	
	210					215					220					
ggt	tcc	tgc	tgc	gca	gag	atg	gat	gtt	tgg	gag	gcc	aat	tcc	atc	tcc	720
Gly	Ser	Cys	Cys	Ala	Glu	Met	Asp	Val	Trp	Glu	Ala	Asn	Ser	Ile	Ser	
225					230				235						240	
gcg	gcc	gta	aca	ccg	cac	tcg	tgc	tcc	aca	acc	agc	cag	acg	atg	tgc	768
Ala	Ala	Val	Thr	Pro	His	Ser	Cys	Ser	Thr	Thr	Ser	Gln	Thr	Met	Cys	
				245				250						255		
aac	ggc	gac	tcc	tgc	ggc	ggt	acc	tac	tca	gcc	aca	cga	tac	gct	ggt	816
Asn	Gly	Asp	Ser	Cys	Gly	Gly	Thr	Tyr	Ser	Ala	Thr	Arg	Tyr	Ala	Gly	
			260				265						270			

gtc tgc gat ccc gat ggc tgc gac ttc aac tcc tac cgt atg ggc gac	864
Val Cys Asp Pro Asp Gly Cys Asp Phe Asn Ser Tyr Arg Met Gly Asp	
275 280 285	
acg acc ttc tac ggc aag gga aag acg gtc gat acc agc tcc aag ttc	912
Thr Thr Phe Tyr Gly Lys Gly Lys Thr Val Asp Thr Ser Ser Lys Phe	
290 295 300	
acg gtc gtg acc cag ttc atc acc gac act gga acc gcc tcc ggc tcg	960
Thr Val Val Thr Gln Phe Ile Thr Asp Thr Gly Thr Ala Ser Gly Ser	
305 310 315 320	
ctc acg gag atc cgc cgc ttc tac gtc cag aac gga aag ttg atc ccc	1008
Leu Thr Glu Ile Arg Arg Phe Tyr Val Gln Asn Gly Lys Leu Ile Pro	
325 330 335	
aac tcc cag tcg aag atc tcg ggc gtc act ggc aac tcc atc acc tct	1056
Asn Ser Gln Ser Lys Ile Ser Gly Val Thr Gly Asn Ser Ile Thr Ser	
340 345 350	
gct ttc tgc gac gct cag aag gcg gct ttc ggc gat aac tac acg ttc	1104
Ala Phe Cys Asp Ala Gln Lys Ala Ala Phe Gly Asp Asn Tyr Thr Phe	
355 360 365	
aag gac aag ggc ggc ttc gca tcc atg act act gct atg aag aac gga	1152
Lys Asp Lys Gly Gly Phe Ala Ser Met Thr Thr Ala Met Lys Asn Gly	
370 375 380	
atg gtc ctg gtt atg agt ctt tgg gat gac cac tac gcc aat atg ctc	1200
Met Val Leu Val Met Ser Leu Trp Asp Asp His Tyr Ala Asn Met Leu	
385 390 395 400	
tgg ctt gat agc gac tat ccc act aac gcg gac tcc tcc aag ccg ggt	1248
Trp Leu Asp Ser Asp Tyr Pro Thr Asn Ala Asp Ser Ser Lys Pro Gly	
405 410 415	
gtt gct cgt ggc acc tgc ccg act tct tcc ggc gtg ccc tcg gat gtc	1296
Val Ala Arg Gly Thr Cys Pro Thr Ser Ser Gly Val Pro Ser Asp Val	
420 425 430	
gag act aac aat gca agc gct tcg gtc acg tac tcc aac att aga ttt	1344
Glu Thr Asn Asn Ala Ser Ala Ser Val Thr Tyr Ser Asn Ile Arg Phe	
435 440 445	
gga gat ctc aat tcc act tac acc gcc cag taa	1377
Gly Asp Leu Asn Ser Thr Tyr Thr Ala Gln	
450 455	

<210> 40

<211> 458

<212> PRT

<213> Trichophaea saccata

<400> 40

Met Gln Arg Leu Leu Val Leu Leu Thr Ser Leu Leu Ala Phe Thr Tyr
1 5 10 15

Gly Gln Gln Val Gly Thr Gln Gln Ala Glu Val His Pro Ser Met Thr
20 25 30

Trp	Gln	Gln	Cys	Thr	Lys	Ser	Gly	Gly	Cys	Thr	Thr	Lys	Asn	Gly	Lys
	35						40					45			
Val	Val	Ile	Asp	Ala	Asn	Trp	Arg	Trp	Val	His	Asn	Val	Gly	Gly	Tyr
	50					55					60				
Thr	Asn	Cys	Tyr	Thr	Gly	Asn	Thr	Trp	Asp	Ser	Ser	Leu	Cys	Pro	Asp
65					70					75					80
Asp	Val	Thr	Cys	Ala	Lys	Asn	Cys	Ala	Leu	Asp	Gly	Ala	Asp	Tyr	Ser
				85					90					95	
Gly	Thr	Tyr	Gly	Val	Thr	Ala	Gly	Gly	Asn	Ser	Leu	Lys	Leu	Thr	Phe
			100					105						110	
Val	Thr	Lys	Gly	Gln	Tyr	Ser	Thr	Asn	Val	Gly	Ser	Arg	Leu	Tyr	Met
		115					120					125			
Leu	Ala	Asp	Asp	Ser	Thr	Tyr	Gln	Met	Tyr	Asn	Leu	Leu	Asn	Gln	Glu
	130					135					140				
Phe	Thr	Phe	Asp	Val	Asp	Val	Ser	Asn	Leu	Pro	Cys	Gly	Leu	Asn	Gly
145					150					155					160
Ala	Leu	Tyr	Phe	Val	Ser	Met	Asp	Lys	Asp	Gly	Gly	Met	Ser	Lys	Tyr
				165					170					175	
Ser	Gly	Asn	Lys	Ala	Gly	Ala	Lys	Tyr	Gly	Thr	Gly	Tyr	Cys	Asp	Ser
			180					185					190		
Gln	Cys	Pro	Arg	Asp	Leu	Lys	Phe	Ile	Asn	Gly	Gln	Gly	Asn	Val	Glu
		195					200					205			
Gly	Trp	Lys	Pro	Ser	Ser	Asn	Asp	Ala	Asn	Ala	Gly	Val	Gly	Gly	His
	210					215					220				
Gly	Ser	Cys	Cys	Ala	Glu	Met	Asp	Val	Trp	Glu	Ala	Asn	Ser	Ile	Ser
225					230					235					240
Ala	Ala	Val	Thr	Pro	His	Ser	Cys	Ser	Thr	Thr	Ser	Gln	Thr	Met	Cys
				245					250					255	
Asn	Gly	Asp	Ser	Cys	Gly	Gly	Thr	Tyr	Ser	Ala	Thr	Arg	Tyr	Ala	Gly
			260					265					270		
Val	Cys	Asp	Pro	Asp	Gly	Cys	Asp	Phe	Asn	Ser	Tyr	Arg	Met	Gly	Asp
		275					280					285			
Thr	Thr	Phe	Tyr	Gly	Lys	Gly	Lys	Thr	Val	Asp	Thr	Ser	Ser	Lys	Phe
	290					295					300				
Thr	Val	Val	Thr	Gln	Phe	Ile	Thr	Asp	Thr	Gly	Thr	Ala	Ser	Gly	Ser
305					310					315					320
Leu	Thr	Glu	Ile	Arg	Arg	Phe	Tyr	Val	Gln	Asn	Gly	Lys	Leu	Ile	Pro
				325					330					335	
Asn	Ser	Gln	Ser	Lys	Ile	Ser	Gly	Val	Thr	Gly	Asn	Ser	Ile	Thr	Ser
			340					345					350		
Ala	Phe	Cys	Asp	Ala	Gln	Lys	Ala	Ala	Phe	Gly	Asp	Asn	Tyr	Thr	Phe
		355					360					365			

Lys Asp Lys Gly Gly Phe Ala Ser Met Thr Thr Ala Met Lys Asn Gly
 370 375 380
 Met Val Leu Val Met Ser Leu Trp Asp Asp His Tyr Ala Asn Met Leu
 385 390 395 400
 Trp Leu Asp Ser Asp Tyr Pro Thr Asn Ala Asp Ser Ser Lys Pro Gly
 405 410 415
 Val Ala Arg Gly Thr Cys Pro Thr Ser Ser Gly Val Pro Ser Asp Val
 420 425 430
 Glu Thr Asn Asn Ala Ser Ala Ser Val Thr Tyr Ser Asn Ile Arg Phe
 435 440 445
 Gly Asp Leu Asn Ser Thr Tyr Thr Ala Gln
 450 455

<210> 41
 <211> 1353
 <212> DNA
 <213> Myceliophthora thermophila

<220>
 <221> CDS
 <222> (1)..(1353)
 <223>

<400> 41

atg aag cag tac ctc cag tac ctc gcg gcg acc ctg ccc ctg gtg ggc	48
Met Lys Gln Tyr Leu Gln Tyr Leu Ala Ala Thr Leu Pro Leu Val Gly	
1 5 10 15	
ctg gcc acg gcc cag cag gcg ggt aac ctg cag acc gag act cac ccc	96
Leu Ala Thr Ala Gln Gln Ala Gly Asn Leu Gln Thr Glu Thr His Pro	
20 25 30	
agg ctc act tgg tcc aag tgc acg gcc ccg gga tcc tgc caa cag gtc	144
Arg Leu Thr Trp Ser Lys Cys Thr Ala Pro Gly Ser Cys Gln Gln Val	
35 40 45	
aac ggc gag gtc gtc atc gac tcc aac tgg cgc tgg gtg cac gac gag	192
Asn Gly Glu Val Val Ile Asp Ser Asn Trp Arg Trp Val His Asp Glu	
50 55 60	
aac gcg cag aac tgc tac gac ggc aac cag tgg acc aac gct tgc agc	240
Asn Ala Gln Asn Cys Tyr Asp Gly Asn Gln Trp Thr Asn Ala Cys Ser	
65 70 75 80	
tct gcc acc gac tgc gcc gag aat tgc gcg ctc gag ggt gcc gac tac	288
Ser Ala Thr Asp Cys Ala Glu Asn Cys Ala Leu Glu Gly Ala Asp Tyr	
85 90 95	
cag ggc acc tat ggc gcc tcg acc agc ggc aat gcc ctg acg ctc acc	336
Gln Gly Thr Tyr Gly Ala Ser Thr Ser Gly Asn Ala Leu Thr Leu Thr	
100 105 110	
ttc gtc act aag cac gag tac ggc acc aac att ggc tcg cgc ctc tac	384
Phe Val Thr Lys His Glu Tyr Gly Thr Asn Ile Gly Ser Arg Leu Tyr	

115	120	125	
ctc atg aac ggc gcg aac aag tac cag atg ttc acc ctc aag ggc aac Leu Met Asn Gly Ala Asn Lys Tyr Gln Met Phe Thr Leu Lys Gly Asn 130 135 140			432
gag ctg gcc ttc gac gtc gac ctc tcg gcc gtc gag tgc ggc ctc aac Glu Leu Ala Phe Asp Val Asp Leu Ser Ala Val Glu Cys Gly Leu Asn 145 150 155 160			480
agc gcc ctc tac ttc gtg gcc atg gag gag gat ggc ggt gtg tcg agc Ser Ala Leu Tyr Phe Val Ala Met Glu Glu Asp Gly Gly Val Ser Ser 165 170 175			528
tac ccg acc aac acg gcc ggt gct aag ttc ggc act ggg tac tgc gac Tyr Pro Thr Asn Thr Ala Gly Ala Lys Phe Gly Thr Gly Tyr Cys Asp 180 185 190			576
gcc caa tgc gca cgc gac ctc aag ttc gtc ggc ggc aag ggc aac atc Ala Gln Cys Ala Arg Asp Leu Lys Phe Val Gly Gly Lys Gly Asn Ile 195 200 205			624
gag ggc tgg aag ccg tcc acc aac gat gcc aat gcc ggt gtc ggt cct Glu Gly Trp Lys Pro Ser Thr Asn Asp Ala Asn Ala Gly Val Gly Pro 210 215 220			672
tat ggc ggg tgc tgc gct gag atc gac gtc tgg gag tcg aac aag tat Tyr Gly Gly Cys Cys Ala Glu Ile Asp Val Trp Glu Ser Asn Lys Tyr 225 230 235 240			720
gct ttc gct ttc acc ccg cac ggt tgc gag aac cct aaa tac cac gtc Ala Phe Ala Phe Thr Pro His Gly Cys Glu Asn Pro Lys Tyr His Val 245 250 255			768
tgc gag acc acc aac tgc ggt ggc acc tac tcc gag gac cgc ttc gct Cys Glu Thr Thr Asn Cys Gly Gly Thr Tyr Ser Glu Asp Arg Phe Ala 260 265 270			816
ggt gac tgc gat gcc aac ggc tgc gac tac aac ccc tac cgc atg ggc Gly Asp Cys Asp Ala Asn Gly Cys Asp Tyr Asn Pro Tyr Arg Met Gly 275 280 285			864
aac cag gac ttc tac ggt ccc ggc ttg acg gtc gat acc agc aag aag Asn Gln Asp Phe Tyr Gly Pro Gly Leu Thr Val Asp Thr Ser Lys Lys 290 295 300			912
ttc acc gtc gtc agc cag ttc gag gag aac aag ctc acc cag ttc ttc Phe Thr Val Val Ser Gln Phe Glu Glu Asn Lys Leu Thr Gln Phe Phe 305 310 315 320			960
gtc cag gac ggc aag aag att gag atc ccc ggc ccc aag gtc gag ggc Val Gln Asp Gly Lys Lys Ile Glu Ile Pro Gly Pro Lys Val Glu Gly 325 330 335			1008
atc gat gcg gac agc gcc gct atc acc cct gag ctg tgc agt gcc ctg Ile Asp Ala Asp Ser Ala Ala Ile Thr Pro Glu Leu Cys Ser Ala Leu 340 345 350			1056
ttc aag gcc ttc gat gac cgt gac cgc ttc tcg gag gtt ggc ggc ttc Phe Lys Ala Phe Asp Asp Arg Asp Arg Phe Ser Glu Val Gly Gly Phe 355 360 365			1104

gat gcc atc aac acg gcc ctc agc act ccc atg gtc ctc gtc atg tcc 1152
 Asp Ala Ile Asn Thr Ala Leu Ser Thr Pro Met Val Leu Val Met Ser
 370 375 380

 atc tgg gat gat cac tac gcc aat atg ctc tgg ctc gac tcg agc tac 1200
 Ile Trp Asp Asp His Tyr Ala Asn Met Leu Trp Leu Asp Ser Ser Tyr
 385 390 395 400

 ccc cct gag aag gct ggc cag cct ggc ggt gac cgt ggc ccg tgt cct 1248
 Pro Pro Glu Lys Ala Gly Gln Pro Gly Gly Asp Arg Gly Pro Cys Pro
 405 410 415

 cag gac tct ggc gtc ccg gcc gac gtt gag gct cag tac cct aat gcc 1296
 Gln Asp Ser Gly Val Pro Ala Asp Val Glu Ala Gln Tyr Pro Asn Ala
 420 425 430

 aag gtc atc tgg tcc aac atc cgc ttc ggc ccc atc ggc tcg act gtc 1344
 Lys Val Ile Trp Ser Asn Ile Arg Phe Gly Pro Ile Gly Ser Thr Val
 435 440 445

 aac gtc taa 1353
 Asn Val
 450

<210> 42
 <211> 450
 <212> PRT
 <213> Myceliophthora thermophila

<400> 42

Met Lys Gln Tyr Leu Gln Tyr Leu Ala Ala Thr Leu Pro Leu Val Gly
 1 5 10 15

 Leu Ala Thr Ala Gln Gln Ala Gly Asn Leu Gln Thr Glu Thr His Pro
 20 25 30

 Arg Leu Thr Trp Ser Lys Cys Thr Ala Pro Gly Ser Cys Gln Gln Val
 35 40 45

 Asn Gly Glu Val Val Ile Asp Ser Asn Trp Arg Trp Val His Asp Glu
 50 55 60

 Asn Ala Gln Asn Cys Tyr Asp Gly Asn Gln Trp Thr Asn Ala Cys Ser
 65 70 75 80

 Ser Ala Thr Asp Cys Ala Glu Asn Cys Ala Leu Glu Gly Ala Asp Tyr
 85 90 95

 Gln Gly Thr Tyr Gly Ala Ser Thr Ser Gly Asn Ala Leu Thr Leu Thr
 100 105 110

 Phe Val Thr Lys His Glu Tyr Gly Thr Asn Ile Gly Ser Arg Leu Tyr
 115 120 125

 Leu Met Asn Gly Ala Asn Lys Tyr Gln Met Phe Thr Leu Lys Gly Asn
 130 135 140

 Glu Leu Ala Phe Asp Val Asp Leu Ser Ala Val Glu Cys Gly Leu Asn
 145 150 155 160

Ser Ala Leu Tyr Phe Val Ala Met Glu Glu Asp Gly Gly Val Ser Ser
 165 170 175
 Tyr Pro Thr Asn Thr Ala Gly Ala Lys Phe Gly Thr Gly Tyr Cys Asp
 180 185 190
 Ala Gln Cys Ala Arg Asp Leu Lys Phe Val Gly Gly Lys Gly Asn Ile
 195 200 205
 Glu Gly Trp Lys Pro Ser Thr Asn Asp Ala Asn Ala Gly Val Gly Pro
 210 215 220
 Tyr Gly Gly Cys Cys Ala Glu Ile Asp Val Trp Glu Ser Asn Lys Tyr
 225 230 235 240
 Ala Phe Ala Phe Thr Pro His Gly Cys Glu Asn Pro Lys Tyr His Val
 245 250 255
 Cys Glu Thr Thr Asn Cys Gly Gly Thr Tyr Ser Glu Asp Arg Phe Ala
 260 265 270
 Gly Asp Cys Asp Ala Asn Gly Cys Asp Tyr Asn Pro Tyr Arg Met Gly
 275 280 285
 Asn Gln Asp Phe Tyr Gly Pro Gly Leu Thr Val Asp Thr Ser Lys Lys
 290 295 300
 Phe Thr Val Val Ser Gln Phe Glu Glu Asn Lys Leu Thr Gln Phe Phe
 305 310 315 320
 Val Gln Asp Gly Lys Lys Ile Glu Ile Pro Gly Pro Lys Val Glu Gly
 325 330 335
 Ile Asp Ala Asp Ser Ala Ala Ile Thr Pro Glu Leu Cys Ser Ala Leu
 340 345 350
 Phe Lys Ala Phe Asp Asp Arg Asp Arg Phe Ser Glu Val Gly Gly Phe
 355 360 365
 Asp Ala Ile Asn Thr Ala Leu Ser Thr Pro Met Val Leu Val Met Ser
 370 375 380
 Ile Trp Asp Asp His Tyr Ala Asn Met Leu Trp Leu Asp Ser Ser Tyr
 385 390 395 400
 Pro Pro Glu Lys Ala Gly Gln Pro Gly Gly Asp Arg Gly Pro Cys Pro
 405 410 415
 Gln Asp Ser Gly Val Pro Ala Asp Val Glu Ala Gln Tyr Pro Asn Ala
 420 425 430
 Lys Val Ile Trp Ser Asn Ile Arg Phe Gly Pro Ile Gly Ser Thr Val
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 Asn Val
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<213> Xylaria hypoxylon

<220>

<221> CDS

<222> (1)..(1341)

<223>

<400> 43

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cag cag gtt gga aag gag caa tct gag act cac cct aag ctg tct tgg	96
Gln Gln Val Gly Lys Glu Gln Ser Glu Thr His Pro Lys Leu Ser Trp	
20 25 30	
aag aag tgc acc agc ggt ggt tcc tgc acc cag acc aac gct gag gtg	144
Lys Lys Cys Thr Ser Gly Gly Ser Cys Thr Gln Thr Asn Ala Glu Val	
35 40 45	
acc atc gac tct aac tgg cga tgg ctt cac tct ctc gaa ggc act gag	192
Thr Ile Asp Ser Asn Trp Arg Trp Leu His Ser Leu Glu Gly Thr Glu	
50 55 60	
aac tgc tac gat ggt aac aag tgg acc tcg cag tgc agc act ggc gag	240
Asn Cys Tyr Asp Gly Asn Lys Trp Thr Ser Gln Cys Ser Thr Gly Glu	
65 70 75 80	
gac tgc gcc acc aag tgc gcc atc gag ggt gcc gac tac agc aag acc	288
Asp Cys Ala Thr Lys Cys Ala Ile Glu Gly Ala Asp Tyr Ser Lys Thr	
85 90 95	
tac ggt gcc tct act agc ggc gat gct ctt acc ctc aag ttc ctg acc	336
Tyr Gly Ala Ser Thr Ser Gly Asp Ala Leu Thr Leu Lys Phe Leu Thr	
100 105 110	
aag cac gag tac gga acc aac atc ggc tcc cga ttc tac ctt atg aat	384
Lys His Glu Tyr Gly Thr Asn Ile Gly Ser Arg Phe Tyr Leu Met Asn	
115 120 125	
ggt gcc gac aag tac cag acc ttc gac ctc aag ggt aac gag ttc acc	432
Gly Ala Asp Lys Tyr Gln Thr Phe Asp Leu Lys Gly Asn Glu Phe Thr	
130 135 140	
ttc gat gtc gac ctg tcc acc gtc gac tgt ggt ctt aac gcc gct ctt	480
Phe Asp Val Asp Leu Ser Thr Val Asp Cys Gly Leu Asn Ala Ala Leu	
145 150 155 160	
tac ttc gtc gcc atg gag gaa gac ggt ggc atg gct agc tac ccc aac	528
Tyr Phe Val Ala Met Glu Glu Asp Gly Gly Met Ala Ser Tyr Pro Asn	
165 170 175	
aac aag gcc ggt gcc aag tac ggt acc ggt tac tgt gac gct cag tgt	576
Asn Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ala Gln Cys	
180 185 190	
gcc cgt gac ttg aag ttc gtc ggt ggc aag ggc aac gtt gag gga tgg	624
Ala Arg Asp Leu Lys Phe Val Gly Gly Lys Gly Asn Val Glu Gly Trp	
195 200 205	
gag cca tcc acc aac gac gac aac gcc ggt gtt ggc cct tac ggt gcc	672

Glu	Pro	Ser	Thr	Asn	Asp	Asp	Asn	Ala	Gly	Val	Gly	Pro	Tyr	Gly	Ala		
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tgc	tgt	gcc	gaa	atc	gat	gtc	tgg	gag	tcc	aac	tct	cac	tct	ttc	gct		720
Cys	Cys	Ala	Glu	Ile	Asp	Val	Trp	Glu	Ser	Asn	Ser	His	Ser	Phe	Ala		
225					230					235					240		
ttc	acc	cct	cac	cct	tgc	acc	acc	aac	gaa	tac	cac	gtc	tgt	gag	cag		768
Phe	Thr	Pro	His	Pro	Cys	Thr	Thr	Asn	Glu	Tyr	His	Val	Cys	Glu	Gln		
				245					250					255			
gac	gag	tgt	ggc	ggc	acc	tac	tct	gag	gac	cga	ttc	gct	ggc	aag	tgt		816
Asp	Glu	Cys	Gly	Gly	Thr	Tyr	Ser	Glu	Asp	Arg	Phe	Ala	Gly	Lys	Cys		
			260					265					270				
gat	gcc	aac	ggc	tgt	gac	tac	aac	cct	tac	cgc	atg	ggc	aac	acc	gac		864
Asp	Ala	Asn	Gly	Cys	Asp	Tyr	Asn	Pro	Tyr	Arg	Met	Gly	Asn	Thr	Asp		
		275					280					285					
ttc	tac	ggc	cag	ggc	aag	acc	gtc	gac	acc	agc	aag	aaa	ttc	act	gtt		912
Phe	Tyr	Gly	Gln	Gly	Lys	Thr	Val	Asp	Thr	Ser	Lys	Lys	Phe	Thr	Val		
	290					295					300						
gtc	acc	cag	ttc	gcc	gaa	aac	aag	ttg	act	cag	ttc	ttc	gtc	cag	gac		960
Val	Thr	Gln	Phe	Ala	Glu	Asn	Lys	Leu	Thr	Gln	Phe	Phe	Val	Gln	Asp		
305					310					315					320		
ggc	aag	aag	att	gag	atc	ccc	ggc	ccc	aag	att	gac	ggc	ttc	cct	acc		1008
Gly	Lys	Lys	Ile	Glu	Ile	Pro	Gly	Pro	Lys	Ile	Asp	Gly	Phe	Pro	Thr		
				325				330						335			
gat	agc	gcc	atc	acc	ccc	gag	tac	tgc	act	gcc	gaa	ttc	aac	gtt	cta		1056
Asp	Ser	Ala	Ile	Thr	Pro	Glu	Tyr	Cys	Thr	Ala	Glu	Phe	Asn	Val	Leu		
			340					345					350				
gga	gac	cgt	gac	cgc	ttc	agt	gaa	gtt	ggc	ggc	ttc	gac	cag	ctc	aac		1104
Gly	Asp	Arg	Asp	Arg	Phe	Ser	Glu	Val	Gly	Gly	Phe	Asp	Gln	Leu	Asn		
		355					360					365					
aac	gct	ctt	gac	gta	ccc	atg	gtc	ctt	gtc	atg	tcc	atc	tgg	gac	gac		1152
Asn	Ala	Leu	Asp	Val	Pro	Met	Val	Leu	Val	Met	Ser	Ile	Trp	Asp	Asp		
	370					375					380						
cac	tac	gcc	aac	atg	ctt	tgg	ctc	gac	tcc	agc	tac	ccc	cct	gag	aag		1200
His	Tyr	Ala	Asn	Met	Leu	Trp	Leu	Asp	Ser	Ser	Tyr	Pro	Pro	Glu	Lys		
	385				390					395					400		
gct	ggc	cag	ccc	ggc	ggc	gac	cgt	ggc	gac	tgt	gcc	ccc	gac	tcc	ggc		1248
Ala	Gly	Gln	Pro	Gly	Gly	Asp	Arg	Gly	Asp	Cys	Ala	Pro	Asp	Ser	Gly		
				405				410					415				
gtc	ccc	tcc	gac	gtc	gag	gcc	agc	atc	ccc	gat	gcc	aag	gtc	gtc	tgg		1296
Val	Pro	Ser	Asp	Val	Glu	Ala	Ser	Ile	Pro	Asp	Ala	Lys	Val	Val	Trp		
			420					425					430				
tcc	aac	atc	cgc	ttc	ggc	ccc	atc	ggc	tct	act	gtc	gag	gtt	taa			1341
Ser	Asn	Ile	Arg	Phe	Gly	Pro	Ile	Gly	Ser	Thr	Val	Glu	Val				
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<210> 44

<211> 446

<212> PRT

<213> Xylaria hypoxylon

<400> 44

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Met Leu Ser Leu Ala Val Ser Ala Ala Leu Leu Gly Leu Ala Ser Ala
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Gln Gln Val Gly Lys Glu Gln Ser Glu Thr His Pro Lys Leu Ser Trp
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Lys Lys Cys Thr Ser Gly Gly Ser Cys Thr Gln Thr Asn Ala Glu Val
35           40           45

Thr Ile Asp Ser Asn Trp Arg Trp Leu His Ser Leu Glu Gly Thr Glu
50           55           60

Asn Cys Tyr Asp Gly Asn Lys Trp Thr Ser Gln Cys Ser Thr Gly Glu
65           70           75           80

Asp Cys Ala Thr Lys Cys Ala Ile Glu Gly Ala Asp Tyr Ser Lys Thr
85           90           95

Tyr Gly Ala Ser Thr Ser Gly Asp Ala Leu Thr Leu Lys Phe Leu Thr
100          105          110

Lys His Glu Tyr Gly Thr Asn Ile Gly Ser Arg Phe Tyr Leu Met Asn
115          120          125

Gly Ala Asp Lys Tyr Gln Thr Phe Asp Leu Lys Gly Asn Glu Phe Thr
130          135          140

Phe Asp Val Asp Leu Ser Thr Val Asp Cys Gly Leu Asn Ala Ala Leu
145          150          155          160

Tyr Phe Val Ala Met Glu Glu Asp Gly Gly Met Ala Ser Tyr Pro Asn
165          170          175

Asn Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ala Gln Cys
180          185          190

Ala Arg Asp Leu Lys Phe Val Gly Gly Lys Gly Asn Val Glu Gly Trp
195          200          205

Glu Pro Ser Thr Asn Asp Asp Asn Ala Gly Val Gly Pro Tyr Gly Ala
210          215          220

Cys Cys Ala Glu Ile Asp Val Trp Glu Ser Asn Ser His Ser Phe Ala
225          230          235          240

Phe Thr Pro His Pro Cys Thr Thr Asn Glu Tyr His Val Cys Glu Gln
245          250          255

Asp Glu Cys Gly Gly Thr Tyr Ser Glu Asp Arg Phe Ala Gly Lys Cys
260          265          270

Asp Ala Asn Gly Cys Asp Tyr Asn Pro Tyr Arg Met Gly Asn Thr Asp
275          280          285

Phe Tyr Gly Gln Gly Lys Thr Val Asp Thr Ser Lys Lys Phe Thr Val
290          295          300

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Val Thr Gln Phe Ala Glu Asn Lys Leu Thr Gln Phe Phe Val Gln Asp
 305 310 315 320

Gly Lys Lys Ile Glu Ile Pro Gly Pro Lys Ile Asp Gly Phe Pro Thr
 325 330 335

Asp Ser Ala Ile Thr Pro Glu Tyr Cys Thr Ala Glu Phe Asn Val Leu
 340 345 350

Gly Asp Arg Asp Arg Phe Ser Glu Val Gly Gly Phe Asp Gln Leu Asn
 355 360 365

Asn Ala Leu Asp Val Pro Met Val Leu Val Met Ser Ile Trp Asp Asp
 370 375 380

His Tyr Ala Asn Met Leu Trp Leu Asp Ser Ser Tyr Pro Pro Glu Lys
 385 390 395 400

Ala Gly Gln Pro Gly Gly Asp Arg Gly Asp Cys Ala Pro Asp Ser Gly
 405 410 415

Val Pro Ser Asp Val Glu Ala Ser Ile Pro Asp Ala Lys Val Val Trp
 420 425 430

Ser Asn Ile Arg Phe Gly Pro Ile Gly Ser Thr Val Glu Val
 435 440 445

<210> 45
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 <212> DNA
 <213> Exidia glandulosa

<220>
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 <222> (1)..(1584)
 <223>

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 Met Tyr Ala Lys Phe Ala Thr Leu Ala Ala Leu Val Ala Ala Ala Ser
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gcc cag cag gca tgc aca ctc acc gcc gag aac cat ccc tcc atg act 96
 Ala Gln Gln Ala Cys Thr Leu Thr Ala Glu Asn His Pro Ser Met Thr
 20 25 30

tgg tct aag tgt gcc gcc gga ggt agc tgc act tcg gtt tct ggt tca 144
 Trp Ser Lys Cys Ala Ala Gly Gly Ser Cys Thr Ser Val Ser Gly Ser
 35 40 45

gtc acc atc gat gcc aac tgg cga tgg ctt cac cag ctc aac agc gcc 192
 Val Thr Ile Asp Ala Asn Trp Arg Trp Leu His Gln Leu Asn Ser Ala
 50 55 60

acc aac tgc tac gac ggc aac aag tgg aac acc acc tac tgc agc aca 240
 Thr Asn Cys Tyr Asp Gly Asn Lys Trp Asn Thr Thr Tyr Cys Ser Thr
 65 70 75 80

gat gct act tgc gct gct cag tgc tgt gtt gat ggc tca gac tat gct 288
 Asp Ala Thr Cys Ala Ala Gln Cys Cys Val Asp Gly Ser Asp Tyr Ala

85								90				95				
ggc	acc	tac	ggt	gcc	acc	act	agc	ggt	aac	gct	ctg	aac	ctc	aag	ttc	336
Gly	Thr	Tyr	Gly	Ala	Thr	Thr	Ser	Gly	Asn	Ala	Leu	Asn	Leu	Lys	Phe	
			100					105					110			
gtc	acc	caa	ggg	tcc	tat	tct	aag	aac	atc	ggt	tcc	cgg	ttg	tac	ctc	384
Val	Thr	Gln	Gly	Ser	Tyr	Ser	Lys	Asn	Ile	Gly	Ser	Arg	Leu	Tyr	Leu	
		115					120					125				
atg	gag	tcg	gat	acc	aag	tat	cag	atg	ttt	caa	ctg	ctc	ggc	cag	gag	432
Met	Glu	Ser	Asp	Thr	Lys	Tyr	Gln	Met	Phe	Gln	Leu	Leu	Gly	Gln	Glu	
	130					135					140					
ttc	act	ttc	gac	gta	gat	gtc	tcc	aac	ttg	ggc	tgc	ggt	ctc	aac	ggt	480
Phe	Thr	Phe	Asp	Val	Asp	Val	Ser	Asn	Leu	Gly	Cys	Gly	Leu	Asn	Gly	
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gcc	ctc	tac	ttc	gtc	agc	atg	gac	gct	gac	ggt	ggc	acg	tcc	aag	tat	528
Ala	Leu	Tyr	Phe	Val	Ser	Met	Asp	Ala	Asp	Gly	Gly	Thr	Ser	Lys	Tyr	
				165					170					175		
acc	ggc	aac	aag	gcc	ggc	gcc	aag	tat	ggc	act	ggc	tac	tgc	gac	agc	576
Thr	Gly	Asn	Lys	Ala	Gly	Ala	Lys	Tyr	Gly	Thr	Gly	Tyr	Cys	Asp	Ser	
			180					185					190			
cag	tgc	ccg	cgc	gac	ctg	aag	ttc	atc	aat	ggt	cag	gcc	aac	gtc	gag	624
Gln	Cys	Pro	Arg	Asp	Leu	Lys	Phe	Ile	Asn	Gly	Gln	Ala	Asn	Val	Glu	
		195					200					205				
ggc	tgg	act	cct	tcc	acc	aac	gat	gcc	aac	gcc	ggc	att	ggc	acc	cac	672
Gly	Trp	Thr	Pro	Ser	Thr	Asn	Asp	Ala	Asn	Ala	Gly	Ile	Gly	Thr	His	
	210					215					220					
ggc	tcc	tgc	tgt	tcg	gag	atg	gac	atc	tgg	gag	gct	aac	aat	gtt	gcc	720
Gly	Ser	Cys	Cys	Ser	Glu	Met	Asp	Ile	Trp	Glu	Ala	Asn	Asn	Val	Ala	
225					230					235					240	
gct	gcg	tac	acc	ccc	cat	cct	tgc	aca	act	atc	ggc	cag	tcg	atc	tgc	768
Ala	Ala	Tyr	Thr	Pro	His	Pro	Cys	Thr	Thr	Ile	Gly	Gln	Ser	Ile	Cys	
				245					250					255		
tcg	ggc	gat	tct	tgc	gga	gga	acc	tac	agc	tct	gac	cgt	tac	gcc	ggt	816
Ser	Gly	Asp	Ser	Cys	Gly	Gly	Thr	Tyr	Ser	Ser	Asp	Arg	Tyr	Ala	Gly	
			260					265					270			
gtc	tgc	gat	cca	gac	ggt	tgc	gat	ttc	aac	agc	tac	cgc	atg	ggc	gac	864
Val	Cys	Asp	Pro	Asp	Gly	Cys	Asp	Phe	Asn	Ser	Tyr	Arg	Met	Gly	Asp	
		275					280					285				
acg	ggc	ttc	tac	ggc	aag	ggc	ctg	aca	gtc	gac	acg	agc	tcc	aag	ttc	912
Thr	Gly	Phe	Tyr	Gly	Lys	Gly	Leu	Thr	Val	Asp	Thr	Ser	Ser	Lys	Phe	
	290					295					300					
acc	gtc	gtc	acc	cag	ttc	ctc	acc	ggc	tcc	gac	ggc	aac	ctt	tcc	gag	960
Thr	Val	Val	Thr	Gln	Phe	Leu	Thr	Gly	Ser	Asp	Gly	Asn	Leu	Ser	Glu	
305					310					315					320	
atc	aag	cgc	ttc	tac	gtc	cag	aac	ggc	aag	gtc	att	ccc	aac	tcg	cag	1008
Ile	Lys	Arg	Phe	Tyr	Val	Gln	Asn	Gly	Lys	Val	Ile	Pro	Asn	Ser	Gln	
				325					330					335		

tcc aag att gcc ggc gtc agc ggc aac tcc atc acc acc gac ttc tgc 1056
 Ser Lys Ile Ala Gly Val Ser Gly Asn Ser Ile Thr Thr Asp Phe Cys
 340 345 350

tcc gcc cag aag acc gcc ttc ggc gac acc aac gtc ttc gcg caa aag 1104
 Ser Ala Gln Lys Thr Ala Phe Gly Asp Thr Asn Val Phe Ala Gln Lys
 355 360 365

gga ggt ctc gcc ggg atg ggc gcc gcc ctc aag gcc ggc atg gtc ctc 1152
 Gly Gly Leu Ala Gly Met Gly Ala Ala Leu Lys Ala Gly Met Val Leu
 370 375 380

gtc atg tcc atc tgg gac gac cac gca gtc aac atg ctg tgg ctg gac 1200
 Val Met Ser Ile Trp Asp Asp His Ala Val Asn Met Leu Trp Leu Asp
 385 390 395 400

tcg acc tac ccg acc gac agc acc aag ccc ggc gcg gcc cgc ggc acc 1248
 Ser Thr Tyr Pro Thr Asp Ser Thr Lys Pro Gly Ala Ala Arg Gly Thr
 405 410 415

tgc ccg acc acc tcc ggc gtc ccc gcc gac gtc gag gcc cag gtc ccc 1296
 Cys Pro Thr Thr Ser Gly Val Pro Ala Asp Val Glu Ala Gln Val Pro
 420 425 430

aac tcg aac gtc atc tac tcc aac atc aag gtc ggc ccc atc aac tcg 1344
 Asn Ser Asn Val Ile Tyr Ser Asn Ile Lys Val Gly Pro Ile Asn Ser
 435 440 445

act ttc acc ggc ggc act tcc ggc ggc ggc ggt agc agc agc agc tcc 1392
 Thr Phe Thr Gly Gly Thr Ser Gly Gly Gly Gly Ser Ser Ser Ser Ser
 450 455 460

acc acc atc cga acc agc acc acc agc act cgc acc acc agc acc agc 1440
 Thr Thr Ile Arg Thr Ser Thr Thr Ser Thr Arg Thr Thr Ser Thr Ser
 465 470 475 480

acc gcg ccc ggc ggc ggc tcc act ggc agc gcc ggc gcc gat cac tgg 1488
 Thr Ala Pro Gly Gly Gly Ser Thr Gly Ser Ala Gly Ala Asp His Trp
 485 490 495

gcg caa tgc ggc ggt atc ggc tgg act ggt ccc acg acc tgc aag agc 1536
 Ala Gln Cys Gly Gly Ile Gly Trp Thr Gly Pro Thr Thr Cys Lys Ser
 500 505 510

ccg tac acg tgc aca gcc tcc aac ccg tac tac tcg cag tgc ttg taa 1584
 Pro Tyr Thr Cys Thr Ala Ser Asn Pro Tyr Tyr Ser Gln Cys Leu
 515 520 525

<210> 46
 <211> 527
 <212> PRT
 <213> Exidia glandulosa

<400> 46

Met Tyr Ala Lys Phe Ala Thr Leu Ala Ala Leu Val Ala Ala Ala Ser
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Ala Gln Gln Ala Cys Thr Leu Thr Ala Glu Asn His Pro Ser Met Thr
 20 25 30

57

Gly Gly Leu Ala Gly Met Gly Ala Ala Leu Lys Ala Gly Met Val Leu
 370 375 380
 Val Met Ser Ile Trp Asp Asp His Ala Val Asn Met Leu Trp Leu Asp
 385 390 395 400
 Ser Thr Tyr Pro Thr Asp Ser Thr Lys Pro Gly Ala Ala Arg Gly Thr
 405 410 415
 Cys Pro Thr Thr Ser Gly Val Pro Ala Asp Val Glu Ala Gln Val Pro
 420 425 430
 Asn Ser Asn Val Ile Tyr Ser Asn Ile Lys Val Gly Pro Ile Asn Ser
 435 440 445
 Thr Phe Thr Gly Gly Thr Ser Gly Gly Gly Gly Ser Ser Ser Ser Ser
 450 455 460
 Thr Thr Ile Arg Thr Ser Thr Thr Ser Thr Arg Thr Thr Ser Thr Ser
 465 470 475 480
 Thr Ala Pro Gly Gly Gly Ser Thr Gly Ser Ala Gly Ala Asp His Trp
 485 490 495
 Ala Gln Cys Gly Gly Ile Gly Trp Thr Gly Pro Thr Thr Cys Lys Ser
 500 505 510
 Pro Tyr Thr Cys Thr Ala Ser Asn Pro Tyr Tyr Ser Gln Cys Leu
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<210> 47
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 <213> Exidia glandulosa

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gcc cag cag gca tgc aca ctc acc gcc gag aac cat ccc tcc atg act	96
Ala Gln Gln Ala Cys Thr Leu Thr Ala Glu Asn His Pro Ser Met Thr	
20 25 30	
tgg tct aag tgt gcc gcc gga ggt agc tgc act tcg gtt tct ggt tca	144
Trp Ser Lys Cys Ala Ala Gly Gly Ser Cys Thr Ser Val Ser Gly Ser	
35 40 45	
gtc acc atc gat gcc aac tgg cga tgg ctt cac cag ctc aac agc gcc	192
Val Thr Ile Asp Ala Asn Trp Arg Trp Leu His Gln Leu Asn Ser Ala	
50 55 60	
acc aac tgc tac gac ggc aac aag tgg aac acc acc tac tgc agc aca	240
Thr Asn Cys Tyr Asp Gly Asn Lys Trp Asn Thr Thr Tyr Cys Ser Thr	

65	70					75					80					
gat gct act tgc gct gct cag tgc tgt gtt gat ggc tca gac tat gct	Asp Ala Thr Cys Ala Ala Gln Cys Cys Val Asp Gly Ser Asp Tyr Ala															288
	85					90					95					
ggc acc tac ggt gcc acc act agc ggt aac gct ctg aac ctc aag ttc	Gly Thr Tyr Gly Ala Thr Thr Ser Gly Asn Ala Leu Asn Leu Lys Phe															336
	100					105					110					
gtc acc caa ggg tcc tat tct aag aac atc ggt tcc cgg ttg tac ctc	Val Thr Gln Gly Ser Tyr Ser Lys Asn Ile Gly Ser Arg Leu Tyr Leu															384
	115					120					125					
atg gag tcg gat acc aag tat cag atg ttt caa ctg ctc ggc cag gag	Met Glu Ser Asp Thr Lys Tyr Gln Met Phe Gln Leu Leu Gly Gln Glu															432
	130					135					140					
ttc act ttc gac gta gat gtc tcc aac ttg ggc tgc ggt ctc aac ggt	Phe Thr Phe Asp Val Asp Val Ser Asn Leu Gly Cys Gly Leu Asn Gly															480
	145					150					155					
gcc ctc tac ttc gtc agc atg gac gct gac ggt ggc acg tcc aag tat	Ala Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Thr Ser Lys Tyr															528
	165					170					175					
acc ggc aac aag gcc ggc gcc aag tat ggc act ggc tac tgc gac agc	Thr Gly Asn Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ser															576
	180					185					190					
cag tgc ccg cgc gac ctg aag ttc atc aat ggt cag gcc aac gtc gag	Gln Cys Pro Arg Asp Leu Lys Phe Ile Asn Gly Gln Ala Asn Val Glu															624
	195					200					205					
ggc tgg act cct tcc acc aac gat gcc aac gcc ggc att ggc acc cac	Gly Trp Thr Pro Ser Thr Asn Asp Ala Asn Ala Gly Ile Gly Thr His															672
	210					215					220					
ggc tcc tgc tgt tcg gag atg gac atc tgg gag gct aac aat gtt gcc	Gly Ser Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Asn Val Ala															720
	225					230					235					
gct gcg tac acc ccc cat cct tgc aca act atc ggc cag tcg atc tgc	Ala Ala Tyr Thr Pro His Pro Cys Thr Thr Ile Gly Gln Ser Ile Cys															768
	245					250					255					
tcg ggc gat tct tgc gga gga acc tac agc tct gac cgt tac gcc ggt	Ser Gly Asp Ser Cys Gly Gly Thr Tyr Ser Ser Asp Arg Tyr Ala Gly															816
	260					265					270					
gtc tgc gat cca gac ggt tgc gat ttc aac agc tac cgc atg ggc gac	Val Cys Asp Pro Asp Gly Cys Asp Phe Asn Ser Tyr Arg Met Gly Asp															864
	275					280					285					
acg ggc ttc tac ggc aag ggc ctg aca gtc gac acg agc tcc aag ttc	Thr Gly Phe Tyr Gly Lys Gly Leu Thr Val Asp Thr Ser Ser Lys Phe															912
	290					295					300					
acc gtc gtc acc cag ttc ctc acc ggc tcc gac ggc aac ctt tcc gag	Thr Val Val Thr Gln Phe Leu Thr Gly Ser Asp Gly Asn Leu Ser Glu															960
	305					310					315					
											320					

atc aag cgc ttc tac gtc cag aac ggc aag gtc att ccc aac tcg cag 1008
 Ile Lys Arg Phe Tyr Val Gln Asn Gly Lys Val Ile Pro Asn Ser Gln
 325 330 335

 tcc aag att gcc ggc gtc agc ggc aac tcc atc acc acc gac ttc tgc 1056
 Ser Lys Ile Ala Gly Val Ser Gly Asn Ser Ile Thr Thr Asp Phe Cys
 340 345 350

 tcc gcc cag aag acc gcc ttc ggc gac acc aac gtc ttc gcg caa aag 1104
 Ser Ala Gln Lys Thr Ala Phe Gly Asp Thr Asn Val Phe Ala Gln Lys
 355 360 365

 gga ggt ctc gcc ggg atg ggc gcc gcc ctc aag gcc ggc atg gtc ctc 1152
 Gly Gly Leu Ala Gly Met Gly Ala Ala Leu Lys Ala Gly Met Val Leu
 370 375 380

 gtc atg tcc atc tgg gac gat cac tac gcc aac atg ctg tgg ctc gac 1200
 Val Met Ser Ile Trp Asp Asp His Tyr Ala Asn Met Leu Trp Leu Asp
 385 390 395 400

 tcg acc tac ccg act gac gcc tct ccc gat gag ccc ggc aag ggc cgc 1248
 Ser Thr Tyr Pro Thr Asp Ala Ser Pro Asp Glu Pro Gly Lys Gly Arg
 405 410 415

 ggc acc tgc gac acc agc tcg ggt gtt cct gct gac atc gag acc agc 1296
 Gly Thr Cys Asp Thr Ser Ser Gly Val Pro Ala Asp Ile Glu Thr Ser
 420 425 430

 cag gcc agc aac tca gtc atc tac tcg aac atc aag ttc gga ccc atc 1344
 Gln Ala Ser Asn Ser Val Ile Tyr Ser Asn Ile Lys Phe Gly Pro Ile
 435 440 445

 aac tcg acc ttc aag gcg tcc taa 1368
 Asn Ser Thr Phe Lys Ala Ser
 450 455

<210> 48
 <211> 455
 <212> PRT
 <213> Exidia glandulosa

<400> 48

Met Tyr Ala Lys Phe Ala Thr Leu Ala Ala Leu Val Ala Ala Ala Ser
 1 5 10 15

 Ala Gln Gln Ala Cys Thr Leu Thr Ala Glu Asn His Pro Ser Met Thr
 20 25 30

 Trp Ser Lys Cys Ala Ala Gly Gly Ser Cys Thr Ser Val Ser Gly Ser
 35 40 45

 Val Thr Ile Asp Ala Asn Trp Arg Trp Leu His Gln Leu Asn Ser Ala
 50 55 60

 Thr Asn Cys Tyr Asp Gly Asn Lys Trp Asn Thr Thr Tyr Cys Ser Thr
 65 70 75 80

 Asp Ala Thr Cys Ala Ala Gln Cys Cys Val Asp Gly Ser Asp Tyr Ala
 85 90 95

Gly	Thr	Tyr	Gly	Ala	Thr	Thr	Ser	Gly	Asn	Ala	Leu	Asn	Leu	Lys	Phe	100	105	110	
Val	Thr	Gln	Gly	Ser	Tyr	Ser	Lys	Asn	Ile	Gly	Ser	Arg	Leu	Tyr	Leu	115	120	125	
Met	Glu	Ser	Asp	Thr	Lys	Tyr	Gln	Met	Phe	Gln	Leu	Leu	Gly	Gln	Glu	130	135	140	
Phe	Thr	Phe	Asp	Val	Asp	Val	Ser	Asn	Leu	Gly	Cys	Gly	Leu	Asn	Gly	145	150	155	160
Ala	Leu	Tyr	Phe	Val	Ser	Met	Asp	Ala	Asp	Gly	Gly	Thr	Ser	Lys	Tyr	165	170	175	
Thr	Gly	Asn	Lys	Ala	Gly	Ala	Lys	Tyr	Gly	Thr	Gly	Tyr	Cys	Asp	Ser	180	185	190	
Gln	Cys	Pro	Arg	Asp	Leu	Lys	Phe	Ile	Asn	Gly	Gln	Ala	Asn	Val	Glu	195	200	205	
Gly	Trp	Thr	Pro	Ser	Thr	Asn	Asp	Ala	Asn	Ala	Gly	Ile	Gly	Thr	His	210	215	220	
Gly	Ser	Cys	Cys	Ser	Glu	Met	Asp	Ile	Trp	Glu	Ala	Asn	Asn	Val	Ala	225	230	235	240
Ala	Ala	Tyr	Thr	Pro	His	Pro	Cys	Thr	Thr	Ile	Gly	Gln	Ser	Ile	Cys	245	250	255	
Ser	Gly	Asp	Ser	Cys	Gly	Gly	Thr	Tyr	Ser	Ser	Asp	Arg	Tyr	Ala	Gly	260	265	270	
Val	Cys	Asp	Pro	Asp	Gly	Cys	Asp	Phe	Asn	Ser	Tyr	Arg	Met	Gly	Asp	275	280	285	
Thr	Gly	Phe	Tyr	Gly	Lys	Gly	Leu	Thr	Val	Asp	Thr	Ser	Ser	Lys	Phe	290	295	300	
Thr	Val	Val	Thr	Gln	Phe	Leu	Thr	Gly	Ser	Asp	Gly	Asn	Leu	Ser	Glu	305	310	315	320
Ile	Lys	Arg	Phe	Tyr	Val	Gln	Asn	Gly	Lys	Val	Ile	Pro	Asn	Ser	Gln	325	330	335	
Ser	Lys	Ile	Ala	Gly	Val	Ser	Gly	Asn	Ser	Ile	Thr	Thr	Asp	Phe	Cys	340	345	350	
Ser	Ala	Gln	Lys	Thr	Ala	Phe	Gly	Asp	Thr	Asn	Val	Phe	Ala	Gln	Lys	355	360	365	
Gly	Gly	Leu	Ala	Gly	Met	Gly	Ala	Ala	Leu	Lys	Ala	Gly	Met	Val	Leu	370	375	380	
Val	Met	Ser	Ile	Trp	Asp	Asp	His	Tyr	Ala	Asn	Met	Leu	Trp	Leu	Asp	385	390	395	400
Ser	Thr	Tyr	Pro	Thr	Asp	Ala	Ser	Pro	Asp	Glu	Pro	Gly	Lys	Gly	Arg	405	410	415	
Gly	Thr	Cys	Asp	Thr	Ser	Ser	Gly	Val	Pro	Ala	Asp	Ile	Glu	Thr	Ser	420	425	430	

Gln Ala Ser Asn Ser Val Ile Tyr Ser Asn Ile Lys Phe Gly Pro Ile
 435 440 445

Asn Ser Thr Phe Lys Ala Ser
 450 455

<210> 49
 <211> 1395
 <212> DNA
 <213> Poitrasia circinans

<220>
 <221> CDS
 <222> (1)..(1395)
 <223>

<400> 49

atg cat cag act tcc gtt ctt tct tcg ctc tct ttg ctc ctc gca gcc	48
Met His Gln Thr Ser Val Leu Ser Ser Leu Ser Leu Leu Leu Ala Ala	
1 5 10 15	
tcc ggt gcc cag cag gtc ggc acc cag aat gct gag act cac ccg agt	96
Ser Gly Ala Gln Gln Val Gly Thr Gln Asn Ala Glu Thr His Pro Ser	
20 25 30	
ctg acc acc cag aag tgt acc acc gac ggc ggc tgc acc gac cag tcc	144
Leu Thr Thr Gln Lys Cys Thr Thr Asp Gly Gly Cys Thr Asp Gln Ser	
35 40 45	
act gcc atc gtg ctt gac gcc aac tgg cgc tgg ctg cac acc acc gag	192
Thr Ala Ile Val Leu Asp Ala Asn Trp Arg Trp Leu His Thr Thr Glu	
50 55 60	
ggc tac acc aac tgc tac act ggc cag gaa tgg gac acc gac atc tgc	240
Gly Tyr Thr Asn Cys Tyr Thr Gly Gln Glu Trp Asp Thr Asp Ile Cys	
65 70 75 80	
tcc tcc ccg gag gct tgc gcc acc ggc tgc gct ctt gac ggt gcc gac	288
Ser Ser Pro Glu Ala Cys Ala Thr Gly Cys Ala Leu Asp Gly Ala Asp	
85 90 95	
tac gag ggc act tac ggc att acg act gac ggc aac gct ctt tcc atg	336
Tyr Glu Gly Thr Tyr Gly Ile Thr Thr Asp Gly Asn Ala Leu Ser Met	
100 105 110	
aag ttt gtc acc cag ggc tcg cag aag aac gtc ggc ggt cgt gtt tac	384
Lys Phe Val Thr Gln Gly Ser Gln Lys Asn Val Gly Gly Arg Val Tyr	
115 120 125	
ctg ctt gct ccc gac tcc gaa gat gcg tac gag ctc ttc aag ttg aag	432
Leu Leu Ala Pro Asp Ser Glu Asp Ala Tyr Glu Leu Phe Lys Leu Lys	
130 135 140	
aac cag gag ttc act ttc gac gtt gac gtc tcc gac ctc ccc tgc ggc	480
Asn Gln Glu Phe Thr Phe Asp Val Asp Val Ser Asp Leu Pro Cys Gly	
145 150 155 160	
ctg aac ggc gcc ctg tac ttc tcc gag atg gat gaa gat ggt ggc atg	528
Leu Asn Gly Ala Leu Tyr Phe Ser Glu Met Asp Glu Asp Gly Gly Met	

165	170	175	
tcc aag tac gag aac aac aag gcc ggc gcc aag tac ggc act ggc tac Ser Lys Tyr Glu Asn Asn Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr 180 185 190			576
tgc gac acg cag tgc ccc cac gac gtc aag ttc atc aac ggc gag gcc Cys Asp Thr Gln Cys Pro His Asp Val Lys Phe Ile Asn Gly Glu Ala 195 200 205			624
aac att ctc aac tgg acc aag tcc gag acc gac gtc aac gcc ggc act Asn Ile Leu Asn Trp Thr Lys Ser Glu Thr Asp Val Asn Ala Gly Thr 210 215 220			672
ggc caa tac ggc tcc tgc tgc aac gag atg gat atc tgg gag gcc aac Gly Gln Tyr Gly Ser Cys Cys Asn Glu Met Asp Ile Trp Glu Ala Asn 225 230 235 240			720
tcg cag gcc acc gcc gtc act ccc cac gtc tgc aac gcc gat gtc atc Ser Gln Ala Thr Ala Val Thr Pro His Val Cys Asn Ala Asp Val Ile 245 250 255			768
ggc cag gtc cgt tgc aac ggc acc gac tgc ggt gac ggc gac aac cgc Gly Gln Val Arg Cys Asn Gly Thr Asp Cys Gly Asp Gly Asp Asn Arg 260 265 270			816
tac ggc ggc gtc tgc gac aag gat ggc tgc gac tac aac ccc tac cgc Tyr Gly Gly Val Cys Asp Lys Asp Gly Cys Asp Tyr Asn Pro Tyr Arg 275 280 285			864
atg ggc aac gag tcg ttc tac ggc tcc aac ggc agc acc atc gac acc Met Gly Asn Glu Ser Phe Tyr Gly Ser Asn Gly Ser Thr Ile Asp Thr 290 295 300			912
act gcc aag ttc acc gtc att acg cag ttc atc acc tcg gac aac act Thr Ala Lys Phe Thr Val Ile Thr Gln Phe Ile Thr Ser Asp Asn Thr 305 310 315 320			960
tcg act ggc gac ctc gtt gag atc cgc cgc aag tac gtc cag gac ggc Ser Thr Gly Asp Leu Val Glu Ile Arg Arg Lys Tyr Val Gln Asp Gly 325 330 335			1008
acc gtc atc gag aac tcg ttc gcc gac tac gac acc ctg gcc acg ttc Thr Val Ile Glu Asn Ser Phe Ala Asp Tyr Asp Thr Leu Ala Thr Phe 340 345 350			1056
aac tcc atc tcg gac gac ttc tgc gac gcc cag aag acg ctc ttc ggc Asn Ser Ile Ser Asp Asp Phe Cys Asp Ala Gln Lys Thr Leu Phe Gly 355 360 365			1104
gac gag aac gac ttc aag acc aag ggc ggc att gcc cgc atg ggc gag Asp Glu Asn Asp Phe Lys Thr Lys Gly Gly Ile Ala Arg Met Gly Glu 370 375 380			1152
tcc ttc gag cgc ggc atg gtc ctc gtc atg agc atc tgg gat gac cac Ser Phe Glu Arg Gly Met Val Leu Val Met Ser Ile Trp Asp Asp His 385 390 395 400			1200
gcg gcc aac gcc ctc tgg ctc gac tcg acc tac ccc gtc gac ggc gac Ala Ala Asn Ala Leu Trp Leu Asp Ser Thr Tyr Pro Val Asp Gly Asp 405 410 415			1248

gcg acc aag cct ggc atc aag cgc ggc cct tgc ggc acc gac act ggt 1296
 Ala Thr Lys Pro Gly Ile Lys Arg Gly Pro Cys Gly Thr Asp Thr Gly
 420 425 430

gtt ccc gcc gac gtc gag tcg gag tcg ccc gat tcg acc gtc atc tac 1344
 Val Pro Ala Asp Val Glu Ser Glu Ser Pro Asp Ser Thr Val Ile Tyr
 435 440 445

tcc aac att cgc tac gga gac att ggc tcc acc ttc aac gcc acc gct 1392
 Ser Asn Ile Arg Tyr Gly Asp Ile Gly Ser Thr Phe Asn Ala Thr Ala
 450 455 460

tag 1395

<210> 50
 <211> 464
 <212> PRT
 <213> Poitrasia circinans

<400> 50

Met His Gln Thr Ser Val Leu Ser Ser Leu Ser Leu Leu Leu Ala Ala
 1 5 10 15

Ser Gly Ala Gln Gln Val Gly Thr Gln Asn Ala Glu Thr His Pro Ser
 20 25 30

Leu Thr Thr Gln Lys Cys Thr Thr Asp Gly Gly Cys Thr Asp Gln Ser
 35 40 45

Thr Ala Ile Val Leu Asp Ala Asn Trp Arg Trp Leu His Thr Thr Glu
 50 55 60

Gly Tyr Thr Asn Cys Tyr Thr Gly Gln Glu Trp Asp Thr Asp Ile Cys
 65 70 75 80

Ser Ser Pro Glu Ala Cys Ala Thr Gly Cys Ala Leu Asp Gly Ala Asp
 85 90 95

Tyr Glu Gly Thr Tyr Gly Ile Thr Thr Asp Gly Asn Ala Leu Ser Met
 100 105 110

Lys Phe Val Thr Gln Gly Ser Gln Lys Asn Val Gly Gly Arg Val Tyr
 115 120 125

Leu Leu Ala Pro Asp Ser Glu Asp Ala Tyr Glu Leu Phe Lys Leu Lys
 130 135 140

Asn Gln Glu Phe Thr Phe Asp Val Asp Val Ser Asp Leu Pro Cys Gly
 145 150 155 160

Leu Asn Gly Ala Leu Tyr Phe Ser Glu Met Asp Glu Asp Gly Gly Met
 165 170 175

Ser Lys Tyr Glu Asn Asn Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr
 180 185 190

Cys Asp Thr Gln Cys Pro His Asp Val Lys Phe Ile Asn Gly Glu Ala
 195 200 205

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Asn Ile Leu Asn Trp Thr Lys Ser Glu Thr Asp Val Asn Ala Gly Thr
 210                      215                      220

Gly Gln Tyr Gly Ser Cys Cys Asn Glu Met Asp Ile Trp Glu Ala Asn
 225                      230                      235                      240

Ser Gln Ala Thr Ala Val Thr Pro His Val Cys Asn Ala Asp Val Ile
                      245                      250                      255

Gly Gln Val Arg Cys Asn Gly Thr Asp Cys Gly Asp Gly Asp Asn Arg
                      260                      265                      270

Tyr Gly Gly Val Cys Asp Lys Asp Gly Cys Asp Tyr Asn Pro Tyr Arg
 275                      280                      285

Met Gly Asn Glu Ser Phe Tyr Gly Ser Asn Gly Ser Thr Ile Asp Thr
 290                      295                      300

Thr Ala Lys Phe Thr Val Ile Thr Gln Phe Ile Thr Ser Asp Asn Thr
 305                      310                      315                      320

Ser Thr Gly Asp Leu Val Glu Ile Arg Arg Lys Tyr Val Gln Asp Gly
                      325                      330                      335

Thr Val Ile Glu Asn Ser Phe Ala Asp Tyr Asp Thr Leu Ala Thr Phe
                      340                      345                      350

Asn Ser Ile Ser Asp Asp Phe Cys Asp Ala Gln Lys Thr Leu Phe Gly
 355                      360                      365

Asp Glu Asn Asp Phe Lys Thr Lys Gly Gly Ile Ala Arg Met Gly Glu
 370                      375                      380

Ser Phe Glu Arg Gly Met Val Leu Val Met Ser Ile Trp Asp Asp His
 385                      390                      395                      400

Ala Ala Asn Ala Leu Trp Leu Asp Ser Thr Tyr Pro Val Asp Gly Asp
                      405                      410                      415

Ala Thr Lys Pro Gly Ile Lys Arg Gly Pro Cys Gly Thr Asp Thr Gly
                      420                      425                      430

Val Pro Ala Asp Val Glu Ser Glu Ser Pro Asp Ser Thr Val Ile Tyr
 435                      440                      445

Ser Asn Ile Arg Tyr Gly Asp Ile Gly Ser Thr Phe Asn Ala Thr Ala
 450                      455                      460

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<210> 51
<211> 1383
<212> DNA
<213> Coprinus cinereus

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<220>
<221> CDS
<222> (1)..(1383)
<223>

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<400> 51

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atg ttc aag aaa gtc gcc ctc acc gct ctc tgc ttc ctc gcc gtc gca

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48

Met 1	Phe	Lys	Lys	Val 5	Ala	Leu	Thr	Ala	Leu 10	Cys	Phe	Leu	Ala	Val 15	Ala	
cag Gln	gcc Ala	caa Gln	cag Gln	gtc Val	ggg Gly	cgc Arg	gaa Glu	gtc Val	gct Ala	gaa Glu	aac Asn	cac His	ccc Pro	cgt Arg	ctc Leu	96
ccg Pro	tgg Trp	cag Gln	cgt Arg	tgc Cys	act Thr	cgc Arg	aac Asn	ggc Gly	gga Gly	tgc Cys	cag Gln	act Thr	gtc Val	tcc Ser	aac Asn	144
ggg Gly	cag Gln	gtc Val	gtc Val	ctc Leu	gac Asp	gcc Ala	aac Asn	tgg Trp	cga Arg	tgg Trp	ctc Leu	cac His	gtc Val	acc Thr	gac Asp	192
ggc Gly	tac Tyr	acc Thr	aac Asn	tgc Cys	tac Tyr	acc Thr	ggg Gly	aac Asn	tcc Ser	tgg Trp	aac Asn	agc Ser	acc Thr	gtc Val	tgc Cys	240
tcc Ser	gac Asp	ccc Pro	acc Thr	acc Thr	tgc Cys	gct Ala	cag Gln	cga Arg	tgc Cys	gct Ala	ctc Leu	gag Glu	ggg Gly	gcc Ala	aac Asn	288
tac Tyr	cag Gln	caa Gln	acc Thr	tac Tyr	ggg Gly	atc Ile	acc Thr	acc Thr	aac Asn	gga Gly	gac Asp	gcc Ala	ctc Leu	acc Thr	atc Ile	336
aag Lys	ttc Phe	ctc Leu	acc Thr	cga Arg	tcc Ser	caa Gln	caa Gln	acc Thr	aac Asn	gtc Val	ggg Gly	gct Ala	cgt Arg	gtc Val	tac Tyr	384
ctc Leu	atg Met	gag Glu	aac Asn	gag Glu	aac Asn	cga Arg	tac Tyr	cag Gln	atg Met	ttc Phe	aac Asn	ctc Leu	ctc Leu	aac Asn	aag Lys	432
gag Glu	ttc Phe	acc Thr	ttc Phe	gac Asp	gtt Val	gac Asp	gtc Val	tcc Ser	aag Lys	gtt Val	cct Pro	tgc Cys	ggg Gly	atc Ile	aac Asn	480
ggg Gly	gcc Ala	ctc Leu	tac Tyr	ttc Phe	atc Ile	cag Gln	atg Met	gac Asp	gcc Ala	gat Asp	ggg Gly	ggg Gly	atg Met	agc Ser	aag Lys	528
caa Gln	ccc Pro	aac Asn	aac Asn	agg Arg	gct Ala	ggg Gly	gct Ala	aag Lys	tac Tyr	ggg Gly	acc Thr	ggc Gly	tac Tyr	tgc Cys	gac Asp	576
tct Ser	cag Gln	tgc Cys	ccc Pro	cgt Arg	gac Asp	atc Ile	aag Lys	ttc Phe	att Ile	gac Asp	ggc Gly	gtg Val	gcc Ala	aac Asn	agc Ser	624
gcc Ala	gac Asp	tgg Trp	act Thr	cca Pro	tcc Ser	gag Glu	acc Thr	gat Asp	ccc Pro	aat Asn	gcc Ala	gga Gly	agg Arg	ggg Gly	cgc Arg	672
tac Tyr	ggc Gly	att Ile	tgc Cys	tgc Cys	gcc Ala	gag Glu	atg Met	gat Asp	atc Ile	tgg Trp	gag Glu	gcc Ala	aac Asn	tcc Ser	atc Ile	720
tcc Ser	aat Asn	gcc Ala	tac Tyr	acc Thr	ccc Pro	cac His	cct Pro	tgc Cys	cga Arg	acc Thr	cag Gln	aac Asn	gat Asp	ggg Gly	ggc Gly	768

tac cag cgc tgc gag ggc cgc gac tgc aac cag cct cgc tat gag ggt 816
 Tyr Gln Arg Cys Glu Gly Arg Asp Cys Asn Gln Pro Arg Tyr Glu Gly
 260 265 270

ctt tgc gat cct gat ggc tgt gac tac aac ccc ttc cgc atg ggt aac 864
 Leu Cys Asp Pro Asp Gly Cys Asp Tyr Asn Pro Phe Arg Met Gly Asn
 275 280 285

aag gac ttc tac gga ccc gga aag acc gtc gac acc aac agg aag atg 912
 Lys Asp Phe Tyr Gly Pro Gly Lys Thr Val Asp Thr Asn Arg Lys Met
 290 295 300

acc gtc gtc acc caa ttc atc acc cac gac aac acc gac act ggc acc 960
 Thr Val Val Thr Gln Phe Ile Thr His Asp Asn Thr Asp Thr Gly Thr
 305 310 315 320

ctc gtt gac atc cgc cgc ctc tac gtt caa gac ggc cgt gtc att gcc 1008
 Leu Val Asp Ile Arg Arg Leu Tyr Val Gln Asp Gly Arg Val Ile Ala
 325 330 335

aac cct ccc acc aac ttc ccc ggt ctc atg ccc gcc cac gac tcc atc 1056
 Asn Pro Pro Thr Asn Phe Pro Gly Leu Met Pro Ala His Asp Ser Ile
 340 345 350

acc gag cag ttc tgc act gac cag aag aac ctc ttc ggc gac tac agc 1104
 Thr Glu Gln Phe Cys Thr Asp Gln Lys Asn Leu Phe Gly Asp Tyr Ser
 355 360 365

agc ttc gct cgt gac ggt ggt ctc gct cac atg ggt cgc tcc ctc gcc 1152
 Ser Phe Ala Arg Asp Gly Gly Leu Ala His Met Gly Arg Ser Leu Ala
 370 375 380

aag ggt cac gtc ctc gct ctc tcc atc tgg aac gac cac ggt gcc cac 1200
 Lys Gly His Val Leu Ala Leu Ser Ile Trp Asn Asp His Gly Ala His
 385 390 395 400

atg ttg tgg ctc gac tcc aac tac ccc acc gac gct gac ccc aac aag 1248
 Met Leu Trp Leu Asp Ser Asn Tyr Pro Thr Asp Ala Asp Pro Asn Lys
 405 410 415

ccc ggt att gct cgt ggt acc tgc ccg acc act ggt ggc acc ccc cgt 1296
 Pro Gly Ile Ala Arg Gly Thr Cys Pro Thr Thr Gly Gly Thr Pro Arg
 420 425 430

gaa acc gaa caa aac cac cct gat gcc cag gtc atc ttc tcc aac att 1344
 Glu Thr Glu Gln Asn His Pro Asp Ala Gln Val Ile Phe Ser Asn Ile
 435 440 445

aaa ttc ggt gac atc ggc tcg act ttc tct ggt tac taa 1383
 Lys Phe Gly Asp Ile Gly Ser Thr Phe Ser Gly Tyr
 450 455 460

<210> 52

<211> 460

<212> PRT

<213> Coprinus cinereus

<400> 52

Met Phe Lys Lys Val Ala Leu Thr Ala Leu Cys Phe Leu Ala Val Ala

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Gln	Ala	Gln	Gln	Val	Gly	Arg	Glu
		20				25	
Ala	Glu	Asn	His	Pro	Arg	Leu	
				30			
Pro	Trp	Gln	Arg	Cys	Thr	Arg	Asn
		35				40	
Gly	Gln	Val	Val	Leu	Asp	Ala	Asn
		50				55	
Trp	Arg	Trp	Leu	His	Val	Thr	Asp
				60			
Gly	Tyr	Thr	Asn	Cys	Tyr	Thr	Gly
				70			
Asn	Ser	Trp	Asn	Ser	Thr	Val	Cys
		75					80
Ser	Asp	Pro	Thr	Thr	Cys	Ala	Gln
				85			
Arg	Cys	Ala	Leu	Glu	Gly	Ala	Asn
						95	
Tyr	Gln	Gln	Thr	Tyr	Gly	Ile	Thr
			100				
Asn	Gly	Asp	Ala	Leu	Thr	Ile	
				110			
Lys	Phe	Leu	Thr	Arg	Ser	Gln	Gln
		115					
Thr	Asn	Val	Gly	Ala	Arg	Val	Tyr
				125			
Leu	Met	Glu	Asn	Glu	Asn	Arg	Tyr
		130				135	
Gln	Met	Phe	Asn	Leu	Leu	Asn	Lys
				140			
Glu	Phe	Thr	Phe	Asp	Val	Asp	Val
				150			
Ser	Lys	Val	Pro	Cys	Gly	Ile	Asn
				155			160
Gly	Ala	Leu	Tyr	Phe	Ile	Gln	Met
				165			
Asp	Ala	Asp	Gly	Gly	Met	Ser	Lys
				170			175
Gln	Pro	Asn	Asn	Arg	Ala	Gly	Ala
			180				
Lys	Tyr	Gly	Thr	Gly	Tyr	Cys	Asp
				185			190
Ser	Gln	Cys	Pro	Arg	Asp	Ile	Lys
		195					
Phe	Ile	Asp	Gly	Val	Ala	Asn	Ser
				200			
Ala	Asp	Trp	Thr	Pro	Ser	Glu	Thr
				210			
Asp	Pro	Asn	Ala	Gly	Arg	Gly	Arg
				215			
Tyr	Gly	Ile	Cys	Cys	Ala	Glu	Met
				220			
Asp	Ile	Trp	Glu	Ala	Asn	Ser	Ile
				225			230
Ser	Asn	Ala	Tyr	Thr	Pro	His	Pro
				235			
Cys	Arg	Thr	Gln	Asn	Asp	Gly	Gly
				240			
Tyr	Gln	Arg	Cys	Glu	Gly	Arg	Asp
			245				
Cys	Asn	Gln	Pro	Arg	Tyr	Glu	Gly
				250			
Leu	Cys	Asp	Pro	Asp	Gly	Cys	Asp
				255			
Tyr	Asn	Pro	Phe	Arg	Met	Gly	Asn
				260			
Lys	Asp	Phe	Tyr	Gly	Pro	Gly	Lys
				265			
Thr	Val	Asp	Thr	Asn	Arg	Lys	Met
				270			
Thr	Val	Val	Thr	Gln	Phe	Ile	Thr
				275			
His	Asp	Asn	Thr	Asp	Thr	Gly	Thr
				280			
Leu	Val	Asp	Ile	Arg	Arg	Leu	Tyr
				285			
Gln	Asp	Gly	Arg	Val	Ile	Ala	
				290			

Asn Pro Pro Thr Asn Phe Pro Gly Leu Met Pro Ala His Asp Ser Ile
 340 345 350
 Thr Glu Gln Phe Cys Thr Asp Gln Lys Asn Leu Phe Gly Asp Tyr Ser
 355 360 365
 Ser Phe Ala Arg Asp Gly Gly Leu Ala His Met Gly Arg Ser Leu Ala
 370 375 380
 Lys Gly His Val Leu Ala Leu Ser Ile Trp Asn Asp His Gly Ala His
 385 390 395 400
 Met Leu Trp Leu Asp Ser Asn Tyr Pro Thr Asp Ala Asp Pro Asn Lys
 405 410 415
 Pro Gly Ile Ala Arg Gly Thr Cys Pro Thr Thr Gly Gly Thr Pro Arg
 420 425 430
 Glu Thr Glu Gln Asn His Pro Asp Ala Gln Val Ile Phe Ser Asn Ile
 435 440 445
 Lys Phe Gly Asp Ile Gly Ser Thr Phe Ser Gly Tyr
 450 455 460

<210> 53
 <211> 1353
 <212> DNA
 <213> Acremonium sp.

<220>
 <221> CDS
 <222> (1)..(1353)
 <223>

<400> 53

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ggc ctt gcc gcg ggc cag caa gcc ggc cgg gag acg ccc gaa aac cac	96
Gly Leu Ala Ala Gly Gln Gln Ala Gly Arg Glu Thr Pro Glu Asn His	
20 25 30	
ccc cgg ctc acc tgg aag aag tgc tcg ggc cag ggg tcc tgc cag acc	144
Pro Arg Leu Thr Trp Lys Lys Cys Ser Gly Gln Gly Ser Cys Gln Thr	
35 40 45	
gtc aac ggc gag gtc gtc att gat gcc aac tgg cgc tgg ctc cac gac	192
Val Asn Gly Glu Val Val Ile Asp Ala Asn Trp Arg Trp Leu His Asp	
50 55 60	
tcc aac atg cag aac tgc tac gac ggc aac cag tgg acc agc gcg tgc	240
Ser Asn Met Gln Asn Cys Tyr Asp Gly Asn Gln Trp Thr Ser Ala Cys	
65 70 75 80	
agc tcg gcc acc gac tgc gcc tcc aag tgc tac atc gag ggt gcc gac	288
Ser Ser Ala Thr Asp Cys Ala Ser Lys Cys Tyr Ile Glu Gly Ala Asp	
85 90 95	
tac ggc agg acc tac ggc gct tcg acg agc ggc gac tcc ctc acg ctc	336

Tyr	Gly	Arg	Thr	Tyr	Gly	Ala	Ser	Thr	Ser	Gly	Asp	Ser	Leu	Thr	Leu	
			100					105					110			
aag	ttt	gtc	act	cag	cac	gag	tac	ggg	acc	aac	atc	ggc	tcg	cgc	ttc	384
Lys	Phe	Val	Thr	Gln	His	Glu	Tyr	Gly	Thr	Asn	Ile	Gly	Ser	Arg	Phe	
		115					120					125				
tac	ctg	atg	agc	agc	ccg	acc	cgg	tac	cag	atg	ttc	acc	ctc	atg	aac	432
Tyr	Leu	Met	Ser	Ser	Pro	Thr	Arg	Tyr	Gln	Met	Phe	Thr	Leu	Met	Asn	
		130				135					140					
aac	gaa	ttt	gct	ttc	gat	gtc	gac	ctc	tcg	acc	gtc	gag	tgc	ggc	atc	480
Asn	Glu	Phe	Ala	Phe	Asp	Val	Asp	Leu	Ser	Thr	Val	Glu	Cys	Gly	Ile	
145					150					155					160	
aac	agc	gcc	ctg	tac	ttc	gtc	gcc	atg	gag	gag	gac	ggc	ggc	atg	gcc	528
Asn	Ser	Ala	Leu	Tyr	Phe	Val	Ala	Met	Glu	Glu	Asp	Gly	Gly	Met	Ala	
				165					170					175		
agc	tac	ccc	acc	aac	aag	gcc	gga	gcc	aag	tac	ggc	acg	ggg	tac	tgc	576
Ser	Tyr	Pro	Thr	Asn	Lys	Ala	Gly	Ala	Lys	Tyr	Gly	Thr	Gly	Tyr	Cys	
			180					185					190			
gac	gcc	caa	tgc	gcc	cgt	gat	ctc	aag	ttc	gtc	ggc	ggc	aag	gcc	aac	624
Asp	Ala	Gln	Cys	Ala	Arg	Asp	Leu	Lys	Phe	Val	Gly	Gly	Lys	Ala	Asn	
		195					200					205				
att	gag	ggc	tgg	agg	ccg	tcc	acc	aac	gac	gcg	aac	gcc	ggc	gtc	ggc	672
Ile	Glu	Gly	Trp	Arg	Pro	Ser	Thr	Asn	Asp	Ala	Asn	Ala	Gly	Val	Gly	
	210					215					220					
ccg	atg	ggc	ggc	tgc	tgc	gcg	gaa	atc	gat	gtt	tgg	gag	tcc	aac	gcc	720
Pro	Met	Gly	Gly	Cys	Cys	Ala	Glu	Ile	Asp	Val	Trp	Glu	Ser	Asn	Ala	
225					230					235					240	
cac	gct	ttt	gcc	ttc	acg	ccg	cac	gcg	tgc	gag	aac	aac	aac	tac	cac	768
His	Ala	Phe	Ala	Phe	Thr	Pro	His	Ala	Cys	Glu	Asn	Asn	Asn	Tyr	His	
				245					250					255		
atc	tgc	gag	acc	tcc	aac	tgc	ggc	ggg	acc	tac	tcc	gac	gac	cgc	ttc	816
Ile	Cys	Glu	Thr	Ser	Asn	Cys	Gly	Gly	Thr	Tyr	Ser	Asp	Asp	Arg	Phe	
			260					265					270			
gcc	ggc	ctc	tgc	gac	gcc	aac	ggc	tgc	gac	tac	aac	ccg	tac	cgc	atg	864
Ala	Gly	Leu	Cys	Asp	Ala	Asn	Gly	Cys	Asp	Tyr	Asn	Pro	Tyr	Arg	Met	
		275					280					285				
ggc	aac	ccc	gac	ttc	tac	ggc	aag	ggc	aag	act	ctt	gac	acc	tcg	cgg	912
Gly	Asn	Pro	Asp	Phe	Tyr	Gly	Lys	Gly	Lys	Thr	Leu	Asp	Thr	Ser	Arg	
	290					295					300					
aag	ttc	acc	gtc	gtc	acc	cgc	ttc	cag	gag	aac	gac	ctc	tcg	cag	tac	960
Lys	Phe	Thr	Val	Val	Thr	Arg	Phe	Gln	Glu	Asn	Asp	Leu	Ser	Gln	Tyr	
305					310					315					320	
ttc	atc	cag	gac	ggc	cgc	aag	atc	gag	atc	ccg	ccc	ccg	acc	tgg	gac	1008
Phe	Ile	Gln	Asp	Gly	Arg	Lys	Ile	Glu	Ile	Pro	Pro	Pro	Thr	Trp	Asp	
				325					330					335		
ggc	ctc	ccg	aag	agc	agc	cac	atc	acg	ccc	gag	ctg	tgc	gcg	acc	cag	1056
Gly	Leu	Pro	Lys	Ser	Ser	His	Ile	Thr	Pro	Glu	Leu	Cys	Ala	Thr	Gln	
			340					345					350			

ttc gac gtc ttc gac gac cgc aac cgc ttc gag gag gtc ggc ggc ttc 1104
 Phe Asp Val Phe Asp Asp Arg Asn Arg Phe Glu Glu Val Gly Gly Phe
 355 360 365
 ccc gcc ctc aac gcc gct ctc cgc atc ccc atg gtc ctt gtc atg tcc 1152
 Pro Ala Leu Asn Ala Ala Leu Arg Ile Pro Met Val Leu Val Met Ser
 370 375 380
 atc tgg gac gac cac tac gcc aac atg ctc tgg ctc gac tcc gtc tac 1200
 Ile Trp Asp Asp His Tyr Ala Asn Met Leu Trp Leu Asp Ser Val Tyr
 385 390 395 400
 ccg ccc gag aag gag ggc acc ccc ggc gcc gag cgt ggc cct tgc ccc 1248
 Pro Pro Glu Lys Glu Gly Thr Pro Gly Ala Glu Arg Gly Pro Cys Pro
 405 410 415
 cag acc tct ggt gtc ccc gcc gaa gtc gag gcc cag tac ccc aac gcc 1296
 Gln Thr Ser Gly Val Pro Ala Glu Val Glu Ala Gln Tyr Pro Asn Ala
 420 425 430
 aag gtc gtc tgg tcc aac atc cgc ttc ggc ccc atc ggc tcg acc tac 1344
 Lys Val Val Trp Ser Asn Ile Arg Phe Gly Pro Ile Gly Ser Thr Tyr
 435 440 445
 aac atg taa 1353
 Asn Met
 450

<210> 54
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 <212> PRT
 <213> Acremonium sp.

<400> 54

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 Gly Leu Ala Ala Gly Gln Gln Ala Gly Arg Glu Thr Pro Glu Asn His
 20 25 30
 Pro Arg Leu Thr Trp Lys Lys Cys Ser Gly Gln Gly Ser Cys Gln Thr
 35 40 45
 Val Asn Gly Glu Val Val Ile Asp Ala Asn Trp Arg Trp Leu His Asp
 50 55 60
 Ser Asn Met Gln Asn Cys Tyr Asp Gly Asn Gln Trp Thr Ser Ala Cys
 65 70 75 80
 Ser Ser Ala Thr Asp Cys Ala Ser Lys Cys Tyr Ile Glu Gly Ala Asp
 85 90 95
 Tyr Gly Arg Thr Tyr Gly Ala Ser Thr Ser Gly Asp Ser Leu Thr Leu
 100 105 110
 Lys Phe Val Thr Gln His Glu Tyr Gly Thr Asn Ile Gly Ser Arg Phe
 115 120 125
 Tyr Leu Met Ser Ser Pro Thr Arg Tyr Gln Met Phe Thr Leu Met Asn

130	135	140														
Asn	Glu	Phe	Ala	Phe	Asp	Val	Asp	Leu	Ser	Thr	Val	Glu	Cys	Gly	Ile	
145					150					155					160	
Asn	Ser	Ala	Leu	Tyr	Phe	Val	Ala	Met	Glu	Glu	Asp	Gly	Gly	Met	Ala	
				165					170					175		
Ser	Tyr	Pro	Thr	Asn	Lys	Ala	Gly	Ala	Lys	Tyr	Gly	Thr	Gly	Tyr	Cys	
			180					185					190			
Asp	Ala	Gln	Cys	Ala	Arg	Asp	Leu	Lys	Phe	Val	Gly	Gly	Lys	Ala	Asn	
		195					200					205				
Ile	Glu	Gly	Trp	Arg	Pro	Ser	Thr	Asn	Asp	Ala	Asn	Ala	Gly	Val	Gly	
	210					215					220					
Pro	Met	Gly	Gly	Cys	Cys	Ala	Glu	Ile	Asp	Val	Trp	Glu	Ser	Asn	Ala	
225					230					235					240	
His	Ala	Phe	Ala	Phe	Thr	Pro	His	Ala	Cys	Glu	Asn	Asn	Asn	Tyr	His	
				245					250					255		
Ile	Cys	Glu	Thr	Ser	Asn	Cys	Gly	Gly	Thr	Tyr	Ser	Asp	Asp	Arg	Phe	
			260					265						270		
Ala	Gly	Leu	Cys	Asp	Ala	Asn	Gly	Cys	Asp	Tyr	Asn	Pro	Tyr	Arg	Met	
		275					280					285				
Gly	Asn	Pro	Asp	Phe	Tyr	Gly	Lys	Gly	Lys	Thr	Leu	Asp	Thr	Ser	Arg	
	290					295					300					
Lys	Phe	Thr	Val	Val	Thr	Arg	Phe	Gln	Glu	Asn	Asp	Leu	Ser	Gln	Tyr	
305					310					315					320	
Phe	Ile	Gln	Asp	Gly	Arg	Lys	Ile	Glu	Ile	Pro	Pro	Pro	Thr	Trp	Asp	
				325					330					335		
Gly	Leu	Pro	Lys	Ser	Ser	His	Ile	Thr	Pro	Glu	Leu	Cys	Ala	Thr	Gln	
			340					345					350			
Phe	Asp	Val	Phe	Asp	Asp	Arg	Asn	Arg	Phe	Glu	Glu	Val	Gly	Gly	Phe	
		355					360					365				
Pro	Ala	Leu	Asn	Ala	Ala	Leu	Arg	Ile	Pro	Met	Val	Leu	Val	Met	Ser	
						375					380					
Ile	Trp	Asp	Asp	His	Tyr	Ala	Asn	Met	Leu	Trp	Leu	Asp	Ser	Val	Tyr	
385					390					395					400	
Pro	Pro	Glu	Lys	Glu	Gly	Thr	Pro	Gly	Ala	Glu	Arg	Gly	Pro	Cys	Pro	
				405					410					415		
Gln	Thr	Ser	Gly	Val	Pro	Ala	Glu	Val	Glu	Ala	Gln	Tyr	Pro	Asn	Ala	
			420					425					430			
Lys	Val	Val	Trp	Ser	Asn	Ile	Arg	Phe	Gly	Pro	Ile	Gly	Ser	Thr	Tyr	
		435					440					445				
Asn	Met															
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<210> 55
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 <212> DNA
 <213> Chaetomidium pingtungium

<220>
 <221> CDS
 <222> (1)..(1599)
 <223>

<400> 55

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Met Leu Ala Ser Thr Phe Ser Tyr Arg Met Tyr Lys Thr Ala Leu Ile	
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ctg gcc gcc ctt ctg ggc tct ggc cag gct cag cag gtc ggt act tcc	96
Leu Ala Ala Leu Leu Gly Ser Gly Gln Ala Gln Gln Val Gly Thr Ser	
20 25 30	
cag gcg gaa gtg cat ccg tcc atg acc tgg cag agc tgc acg gct ggc	144
Gln Ala Glu Val His Pro Ser Met Thr Trp Gln Ser Cys Thr Ala Gly	
35 40 45	
ggc agc tgc acc acc aac aac ggc aag gtg gtc atc gac gcg aac tgg	192
Gly Ser Cys Thr Thr Asn Asn Gly Lys Val Val Ile Asp Ala Asn Trp	
50 55 60	
cgt tgg gtg cac aaa gtc ggc gac tac acc aac tgc tac acc ggc aac	240
Arg Trp Val His Lys Val Gly Asp Tyr Thr Asn Cys Tyr Thr Gly Asn	
65 70 75 80	
acc tgg gac acg act atc tgc cct gac gat gcg acc tgc gca tcc aac	288
Thr Trp Asp Thr Thr Ile Cys Pro Asp Asp Ala Thr Cys Ala Ser Asn	
85 90 95	
tgc gcc ctt gag ggt gcc aac tac gaa tcc acc tat ggt gtg acc gcc	336
Cys Ala Leu Glu Gly Ala Asn Tyr Glu Ser Thr Tyr Gly Val Thr Ala	
100 105 110	
agc ggc aat tcc ctc cgc ctc aac ttc gtc acc acc agc cag cag aag	384
Ser Gly Asn Ser Leu Arg Leu Asn Phe Val Thr Thr Ser Gln Gln Lys	
115 120 125	
aac att ggc tcg cgt ctg tac atg atg aag gac gac tcg acc tac gag	432
Asn Ile Gly Ser Arg Leu Tyr Met Met Lys Asp Asp Ser Thr Tyr Glu	
130 135 140	
atg ttt aag ctg ctg aac cag gag ttc acc ttc gat gtc gat gtc tcc	480
Met Phe Lys Leu Leu Asn Gln Glu Phe Thr Phe Asp Val Asp Val Ser	
145 150 155 160	
aac ctc ccc tgc ggt ctc aac ggt gct ctg tac ttt gtc gcc atg gac	528
Asn Leu Pro Cys Gly Leu Asn Gly Ala Leu Tyr Phe Val Ala Met Asp	
165 170 175	
gcc ggc ggt ggc atg tcc aag tac cca acc aac aag gcc ggt gcc aag	576
Ala Gly Gly Gly Met Ser Lys Tyr Pro Thr Asn Lys Ala Gly Ala Lys	
180 185 190	
tac ggt act gga tac tgt gac tcg cag tgc cct cgc gac ctc aag ttc	624

Tyr	Gly	Thr	Gly	Tyr	Cys	Asp	Ser	Gln	Cys	Pro	Arg	Asp	Leu	Lys	Phe	
	195						200					205				
atc	aac	ggt	cag	gcc	aac	gtt	gaa	ggg	tgg	cag	ccc	tcc	tcc	aac	gat	672
Ile	Asn	Gly	Gln	Ala	Asn	Val	Glu	Gly	Trp	Gln	Pro	Ser	Ser	Asn	Asp	
	210					215					220					
gcc	aat	gcg	ggt	acc	ggc	aac	cac	ggg	tcc	tgc	tgc	gcg	gag	atg	gat	720
Ala	Asn	Ala	Gly	Thr	Gly	Asn	His	Gly	Ser	Cys	Cys	Ala	Glu	Met	Asp	
225					230				235						240	
atc	tgg	gag	gcc	aac	agc	atc	tcc	acg	gcc	ttc	acc	ccc	cat	ccg	tgc	768
Ile	Trp	Glu	Ala	Asn	Ser	Ile	Ser	Thr	Ala	Phe	Thr	Pro	His	Pro	Cys	
				245					250					255		
gac	acg	ccc	ggc	cag	gtg	atg	tgc	acc	ggt	gat	gcc	tgc	ggt	ggc	acc	816
Asp	Thr	Pro	Gly	Gln	Val	Met	Cys	Thr	Gly	Asp	Ala	Cys	Gly	Gly	Thr	
			260					265					270			
tac	agc	tcc	gac	cgc	tac	ggc	ggc	acc	tgc	gac	ccc	gac	gga	tgt	gat	864
Tyr	Ser	Ser	Asp	Arg	Tyr	Gly	Gly	Thr	Cys	Asp	Pro	Asp	Gly	Cys	Asp	
		275					280					285				
ttc	aac	tcc	ttc	cgc	cag	ggc	aac	aag	acc	ttc	tac	ggc	cct	ggc	atg	912
Phe	Asn	Ser	Phe	Arg	Gln	Gly	Asn	Lys	Thr	Phe	Tyr	Gly	Pro	Gly	Met	
	290					295					300					
acc	gtc	gac	acc	aag	agc	aag	ttt	acc	gtc	gtc	acc	cag	ttc	atc	acc	960
Thr	Val	Asp	Thr	Lys	Ser	Lys	Phe	Thr	Val	Val	Thr	Gln	Phe	Ile	Thr	
305					310				315						320	
gac	gac	ggc	acc	tcc	agc	ggc	acc	ctc	aag	gag	atc	aag	cgc	ttc	tac	1008
Asp	Asp	Gly	Thr	Ser	Ser	Gly	Thr	Leu	Lys	Glu	Ile	Lys	Arg	Phe	Tyr	
				325				330						335		
gtg	cag	aac	ggc	aag	gtg	atc	ccc	aac	tcg	gag	tcg	acc	tgg	acc	ggc	1056
Val	Gln	Asn	Gly	Lys	Val	Ile	Pro	Asn	Ser	Glu	Ser	Thr	Trp	Thr	Gly	
			340					345					350			
gtc	agc	ggc	aac	tcc	atc	acc	acc	gag	tac	tgc	acc	gcc	cag	aag	agc	1104
Val	Ser	Gly	Asn	Ser	Ile	Thr	Thr	Glu	Tyr	Cys	Thr	Ala	Gln	Lys	Ser	
		355					360					365				
ctg	ttc	cag	gac	cag	aac	gtc	ttc	gaa	aag	cac	ggc	ggc	ctc	gag	ggc	1152
Leu	Phe	Gln	Asp	Gln	Asn	Val	Phe	Glu	Lys	His	Gly	Gly	Leu	Glu	Gly	
	370					375					380					
atg	ggt	gct	gcc	ctc	gcc	cag	ggc	atg	gtt	ctc	gtc	atg	tcc	ctg	tgg	1200
Met	Gly	Ala	Ala	Leu	Ala	Gln	Gly	Met	Val	Leu	Val	Met	Ser	Leu	Trp	
385					390				395						400	
gat	gat	cac	tcg	gcc	aac	atg	ctc	tgg	ctc	gac	agc	aac	tac	ccg	acc	1248
Asp	Asp	His	Ser	Ala	Asn	Met	Leu	Trp	Leu	Asp	Ser	Asn	Tyr	Pro	Thr	
				405				410					415			
act	gcc	tct	tcc	acc	act	ccc	ggc	gtc	gcc	cgt	ggt	acc	tgc	gac	atc	1296
Thr	Ala	Ser	Ser	Thr	Thr	Pro	Gly	Val	Ala	Arg	Gly	Thr	Cys	Asp	Ile	
			420					425					430			
tcc	tcc	ggc	gtc	cct	gcg	gat	gtc	gag	gcg	aac	cac	ccc	gac	gcc	tac	1344
Ser	Ser	Gly	Val	Pro	Ala	Asp	Val	Glu	Ala	Asn	His	Pro	Asp	Ala	Tyr	
		435					440					445				

gtc gtc tac tcc aac atc aag gtc ggc ccc atc ggc tcg acc ttc aac 1392
 Val Val Tyr Ser Asn Ile Lys Val Gly Pro Ile Gly Ser Thr Phe Asn
 450 455 460
 agc ggt ggc tcg aac ccc ggt ggc gga acc acc acg aca act acc acc 1440
 Ser Gly Gly Ser Asn Pro Gly Gly Gly Thr Thr Thr Thr Thr Thr Thr
 465 470 475 480
 cag cct act acc acc acg acc acg gct gga aac cct ggc ggc acc gga 1488
 Gln Pro Thr Thr Thr Thr Thr Thr Ala Gly Asn Pro Gly Gly Thr Gly
 485 490 495
 gtc gca cag cac tat ggc cag tgt ggt gga atc gga tgg acc gga ccc 1536
 Val Ala Gln His Tyr Gly Gln Cys Gly Gly Ile Gly Trp Thr Gly Pro
 500 505 510
 aca acc tgt gcc agc cct tat acc tgc cag aag ctg aat gat tat tac 1584
 Thr Thr Cys Ala Ser Pro Tyr Thr Cys Gln Lys Leu Asn Asp Tyr Tyr
 515 520 525
 tct cag tgc ctg tag 1599
 Ser Gln Cys Leu
 530

<210> 56
 <211> 532
 <212> PRT
 <213> Chaetomidium pingtungium

<400> 56

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 Leu Ala Ala Leu Leu Gly Ser Gly Gln Ala Gln Gln Val Gly Thr Ser
 20 25 30
 Gln Ala Glu Val His Pro Ser Met Thr Trp Gln Ser Cys Thr Ala Gly
 35 40 45
 Gly Ser Cys Thr Thr Asn Asn Gly Lys Val Val Ile Asp Ala Asn Trp
 50 55 60
 Arg Trp Val His Lys Val Gly Asp Tyr Thr Asn Cys Tyr Thr Gly Asn
 65 70 75 80
 Thr Trp Asp Thr Thr Ile Cys Pro Asp Asp Ala Thr Cys Ala Ser Asn
 85 90 95
 Cys Ala Leu Glu Gly Ala Asn Tyr Glu Ser Thr Tyr Gly Val Thr Ala
 100 105 110
 Ser Gly Asn Ser Leu Arg Leu Asn Phe Val Thr Thr Ser Gln Gln Lys
 115 120 125
 Asn Ile Gly Ser Arg Leu Tyr Met Met Lys Asp Asp Ser Thr Tyr Glu
 130 135 140
 Met Phe Lys Leu Leu Asn Gln Glu Phe Thr Phe Asp Val Asp Val Ser
 145 150 155 160

Asn Leu Pro Cys Gly Leu Asn Gly Ala Leu Tyr Phe Val Ala Met Asp
 165 170 175
 Ala Gly Gly Gly Met Ser Lys Tyr Pro Thr Asn Lys Ala Gly Ala Lys
 180 185 190
 Tyr Gly Thr Gly Tyr Cys Asp Ser Gln Cys Pro Arg Asp Leu Lys Phe
 195 200 205
 Ile Asn Gly Gln Ala Asn Val Glu Gly Trp Gln Pro Ser Ser Asn Asp
 210 215 220
 Ala Asn Ala Gly Thr Gly Asn His Gly Ser Cys Cys Ala Glu Met Asp
 225 230 235 240
 Ile Trp Glu Ala Asn Ser Ile Ser Thr Ala Phe Thr Pro His Pro Cys
 245 250 255
 Asp Thr Pro Gly Gln Val Met Cys Thr Gly Asp Ala Cys Gly Gly Thr
 260 265 270
 Tyr Ser Ser Asp Arg Tyr Gly Gly Thr Cys Asp Pro Asp Gly Cys Asp
 275 280 285
 Phe Asn Ser Phe Arg Gln Gly Asn Lys Thr Phe Tyr Gly Pro Gly Met
 290 295 300
 Thr Val Asp Thr Lys Ser Lys Phe Thr Val Val Thr Gln Phe Ile Thr
 305 310 315 320
 Asp Asp Gly Thr Ser Ser Gly Thr Leu Lys Glu Ile Lys Arg Phe Tyr
 325 330 335
 Val Gln Asn Gly Lys Val Ile Pro Asn Ser Glu Ser Thr Trp Thr Gly
 340 345 350
 Val Ser Gly Asn Ser Ile Thr Thr Glu Tyr Cys Thr Ala Gln Lys Ser
 355 360 365
 Leu Phe Gln Asp Gln Asn Val Phe Glu Lys His Gly Gly Leu Glu Gly
 370 375 380
 Met Gly Ala Ala Leu Ala Gln Gly Met Val Leu Val Met Ser Leu Trp
 385 390 395 400
 Asp Asp His Ser Ala Asn Met Leu Trp Leu Asp Ser Asn Tyr Pro Thr
 405 410 415
 Thr Ala Ser Ser Thr Thr Pro Gly Val Ala Arg Gly Thr Cys Asp Ile
 420 425 430
 Ser Ser Gly Val Pro Ala Asp Val Glu Ala Asn His Pro Asp Ala Tyr
 435 440 445
 Val Val Tyr Ser Asn Ile Lys Val Gly Pro Ile Gly Ser Thr Phe Asn
 450 455 460
 Ser Gly Gly Ser Asn Pro Gly Gly Gly Thr Thr Thr Thr Thr Thr Thr
 465 470 475 480
 Gln Pro Thr Thr Thr Thr Thr Thr Ala Gly Asn Pro Gly Gly Thr Gly

485 490 495

Val Ala Gln His Tyr Gly Gln Cys Gly Gly Ile Gly Trp Thr Gly Pro
500 505 510

Thr Thr Cys Ala Ser Pro Tyr Thr Cys Gln Lys Leu Asn Asp Tyr Tyr
515 520 525

Ser Gln Cys Leu
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<210> 57
<211> 1383
<212> DNA
<213> Sporotrichum pruinosum

<220>
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<222> (1)..(1383)
<223>

<400> 57

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cag gcc caa cag gtc ggt cgc gaa gtc gct gaa aac cac ccc cgt ctc	96
Gln Ala Gln Gln Val Gly Arg Glu Val Ala Glu Asn His Pro Arg Leu	
20 25 30	
ccg tgg cag cgt tgc act cgc aac ggc gga tgc cag act gtc tct aac	144
Pro Trp Gln Arg Cys Thr Arg Asn Gly Gly Cys Gln Thr Val Ser Asn	
35 40 45	
ggt cag gtc gtc ctc gac gcc aac tgg cga tgg ctc cac gtc acc gat	192
Gly Gln Val Val Leu Asp Ala Asn Trp Arg Trp Leu His Val Thr Asp	
50 55 60	
ggc tac acc aac tgc tac acc ggt aac tcc tgg aac agc acc gtc tgc	240
Gly Tyr Thr Asn Cys Tyr Thr Gly Asn Ser Trp Asn Ser Thr Val Cys	
65 70 75 80	
tcc gac ccc acc acc tgc gct cag cga tgc gct ctc gag ggt gcc aac	288
Ser Asp Pro Thr Thr Cys Ala Gln Arg Cys Ala Leu Glu Gly Ala Asn	
85 90 95	
tac cag caa acc tac ggt atc acc acc aac gga gac gcc ctc acc atc	336
Tyr Gln Gln Thr Tyr Gly Ile Thr Thr Asn Gly Asp Ala Leu Thr Ile	
100 105 110	
aag ttc ctc acc cga tcc caa caa acc aac gtc ggt gct cgt gtc tac	384
Lys Phe Leu Thr Arg Ser Gln Gln Thr Asn Val Gly Ala Arg Val Tyr	
115 120 125	
ctc atg gag aac gag aac cga tac cag atg ttc aac ctc ctc aac aag	432
Leu Met Glu Asn Glu Asn Arg Tyr Gln Met Phe Asn Leu Leu Asn Lys	
130 135 140	
gag ttc acc ttc gac gtt gac gtc tcc aag gtt cct tgc ggt atc aac	480
Glu Phe Thr Phe Asp Val Asp Val Ser Lys Val Pro Cys Gly Ile Asn	

145	150	155	160	
ggt gcc ctc tac ttc atc cag atg gac gcc gat ggt ggt atg agc aag Gly Ala Leu Tyr Phe Ile Gln Met Asp Ala Asp Gly Gly Met Ser Lys 165 170 175				528
caa ccc aac aac agg gct ggt gct aag tac ggt acc ggc tac tgc gac Gln Pro Asn Asn Arg Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp 180 185 190				576
tct cag tgc ccc cgt gac atc aag ttc att gac ggc gtg gcc aac agc Ser Gln Cys Pro Arg Asp Ile Lys Phe Ile Asp Gly Val Ala Asn Ser 195 200 205				624
gcc gac tgg act cca tcc gag acc gat ccc aat gcc gga agg ggt cgc Ala Asp Trp Thr Pro Ser Glu Thr Asp Pro Asn Ala Gly Arg Gly Arg 210 215 220				672
tac ggc att tgc tgc gcc gag atg gat atc tgg gag gcc aac tcc atc Tyr Gly Ile Cys Cys Ala Glu Met Asp Ile Trp Glu Ala Asn Ser Ile 225 230 235 240				720
tcc aat gcc tac acc ccc cac cct tgc cga acc cag aac gat ggt ggc Ser Asn Ala Tyr Thr Pro His Pro Cys Arg Thr Gln Asn Asp Gly Gly 245 250 255				768
tac cag cgc tgc gag ggc cgc gac tgc aac cag cct cgc tat gag ggt Tyr Gln Arg Cys Glu Gly Arg Asp Cys Asn Gln Pro Arg Tyr Glu Gly 260 265 270				816
ctt tgc gat cct gat ggc tgt gac tac aac ccc ttc cgc atg ggt aac Leu Cys Asp Pro Asp Gly Cys Asp Tyr Asn Pro Phe Arg Met Gly Asn 275 280 285				864
aag gac ttc tac gga ccc gga aag acc atc gac acc aac agg aag atg Lys Asp Phe Tyr Gly Pro Gly Lys Thr Ile Asp Thr Asn Arg Lys Met 290 295 300				912
acc gtc gtc acc caa ttc atc acc cac gac aac acc gac act ggc acc Thr Val Val Thr Gln Phe Ile Thr His Asp Asn Thr Asp Thr Gly Thr 305 310 315 320				960
ctc gtt gac atc cgc cgc ctc tac gtt caa gac ggc cgt gtc att gcc Leu Val Asp Ile Arg Arg Leu Tyr Val Gln Asp Gly Arg Val Ile Ala 325 330 335				1008
aac cct ccc acc aac ttc ccc ggt ctc atg ccc gcc cac gac tcc atc Asn Pro Pro Thr Asn Phe Pro Gly Leu Met Pro Ala His Asp Ser Ile 340 345 350				1056
acc gag cag ttc tgc act gac cag aag aac ctc ttc ggc gac tac agc Thr Glu Gln Phe Cys Thr Asp Gln Lys Asn Leu Phe Gly Asp Tyr Ser 355 360 365				1104
agc ttc gct cgt gac ggt ggt ctc gct cac atg ggt cgc tcc ctc gcc Ser Phe Ala Arg Asp Gly Gly Leu Ala His Met Gly Arg Ser Leu Ala 370 375 380				1152
aag ggt cac gtc ctc gct ctc tcc atc tgg aac gac cac ggt gcc cac Lys Gly His Val Leu Ala Leu Ser Ile Trp Asn Asp His Gly Ala His 385 390 395 400				1200

atg ttg tgg ctc gac tcc aac tac ccc acc gac gct gac ccc aac aag 1248
 Met Leu Trp Leu Asp Ser Asn Tyr Pro Thr Asp Ala Asp Pro Asn Lys
 405 410 415

ccc ggt att gct cgt ggt acc tgc ccg acc act ggt ggc acc ccc cgt 1296
 Pro Gly Ile Ala Arg Gly Thr Cys Pro Thr Thr Gly Gly Thr Pro Arg
 420 425 430

gaa acc gaa caa aac cac cct gat gcc cag gtc atc ttc tcc aac att 1344
 Glu Thr Glu Gln Asn His Pro Asp Ala Gln Val Ile Phe Ser Asn Ile
 435 440 445

aaa ttc ggt gac atc ggc tcg act ttc tct ggt tac taa 1383
 Lys Phe Gly Asp Ile Gly Ser Thr Phe Ser Gly Tyr
 450 455 460

<210> 58

<211> 460

<212> PRT

<213> Sporotrichum pruinosum

<400> 58

Met Phe Lys Lys Val Ala Leu Thr Ala Leu Cys Phe Leu Ala Val Ala
 1 5 10 15

Gln Ala Gln Gln Val Gly Arg Glu Val Ala Glu Asn His Pro Arg Leu
 20 25 30

Pro Trp Gln Arg Cys Thr Arg Asn Gly Gly Cys Gln Thr Val Ser Asn
 35 40 45

Gly Gln Val Val Leu Asp Ala Asn Trp Arg Trp Leu His Val Thr Asp
 50 55 60

Gly Tyr Thr Asn Cys Tyr Thr Gly Asn Ser Trp Asn Ser Thr Val Cys
 65 70 75 80

Ser Asp Pro Thr Thr Cys Ala Gln Arg Cys Ala Leu Glu Gly Ala Asn
 85 90 95

Tyr Gln Gln Thr Tyr Gly Ile Thr Thr Asn Gly Asp Ala Leu Thr Ile
 100 105 110

Lys Phe Leu Thr Arg Ser Gln Gln Thr Asn Val Gly Ala Arg Val Tyr
 115 120 125

Leu Met Glu Asn Glu Asn Arg Tyr Gln Met Phe Asn Leu Leu Asn Lys
 130 135 140

Glu Phe Thr Phe Asp Val Asp Val Ser Lys Val Pro Cys Gly Ile Asn
 145 150 155 160

Gly Ala Leu Tyr Phe Ile Gln Met Asp Ala Asp Gly Gly Met Ser Lys
 165 170 175

Gln Pro Asn Asn Arg Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp
 180 185 190

Ser Gln Cys Pro Arg Asp Ile Lys Phe Ile Asp Gly Val Ala Asn Ser
 195 200 205

Ala Asp Trp Thr Pro Ser Glu Thr Asp Pro Asn Ala Gly Arg Gly Arg
 210 215 220
 Tyr Gly Ile Cys Cys Ala Glu Met Asp Ile Trp Glu Ala Asn Ser Ile
 225 230 235 240
 Ser Asn Ala Tyr Thr Pro His Pro Cys Arg Thr Gln Asn Asp Gly Gly
 245 250 255
 Tyr Gln Arg Cys Glu Gly Arg Asp Cys Asn Gln Pro Arg Tyr Glu Gly
 260 265 270
 Leu Cys Asp Pro Asp Gly Cys Asp Tyr Asn Pro Phe Arg Met Gly Asn
 275 280 285
 Lys Asp Phe Tyr Gly Pro Gly Lys Thr Ile Asp Thr Asn Arg Lys Met
 290 295 300
 Thr Val Val Thr Gln Phe Ile Thr His Asp Asn Thr Asp Thr Gly Thr
 305 310 315 320
 Leu Val Asp Ile Arg Arg Leu Tyr Val Gln Asp Gly Arg Val Ile Ala
 325 330 335
 Asn Pro Pro Thr Asn Phe Pro Gly Leu Met Pro Ala His Asp Ser Ile
 340 345 350
 Thr Glu Gln Phe Cys Thr Asp Gln Lys Asn Leu Phe Gly Asp Tyr Ser
 355 360 365
 Ser Phe Ala Arg Asp Gly Gly Leu Ala His Met Gly Arg Ser Leu Ala
 370 375 380
 Lys Gly His Val Leu Ala Leu Ser Ile Trp Asn Asp His Gly Ala His
 385 390 395 400
 Met Leu Trp Leu Asp Ser Asn Tyr Pro Thr Asp Ala Asp Pro Asn Lys
 405 410 415
 Pro Gly Ile Ala Arg Gly Thr Cys Pro Thr Thr Gly Gly Thr Pro Arg
 420 425 430
 Glu Thr Glu Gln Asn His Pro Asp Ala Gln Val Ile Phe Ser Asn Ile
 435 440 445
 Lys Phe Gly Asp Ile Gly Ser Thr Phe Ser Gly Tyr
 450 455 460

<210> 59
 <211> 1578
 <212> DNA
 <213> *Scytalidium thermophilum*

<220>
 <221> CDS
 <222> (1) .. (1578)
 <223>

<400> 59

atg cgt acc gcc aag ttc gcc acc ctc gcc gcc ctt gtg gcc tcg gcc Met Arg Thr Ala Lys Phe Ala Thr Leu Ala Ala Leu Val Ala Ser Ala 1 5 10 15	48
gcc gcc cag cag gcg tgc agt ctc acc acc gag agg cac cct tcc ctc Ala Ala Gln Gln Ala Cys Ser Leu Thr Thr Glu Arg His Pro Ser Leu 20 25 30	96
tct tgg aag aag tgc acc gcc ggc ggc cag tgc cag acc gtc cag gct Ser Trp Lys Lys Cys Thr Ala Gly Gly Gln Cys Gln Thr Val Gln Ala 35 40 45	144
tcc atc act ctc gac tcc aac tgg cgc tgg act cac cag gtg tct ggc Ser Ile Thr Leu Asp Ser Asn Trp Arg Trp Thr His Gln Val Ser Gly 50 55 60	192
tcc acc aac tgc tac acg ggc aac aag tgg gat act agc atc tgc act Ser Thr Asn Cys Tyr Thr Gly Asn Lys Trp Asp Thr Ser Ile Cys Thr 65 70 75 80	240
gat gcc aag tcg tgc gct cag aac tgc tgc gtc gat ggt gcc gac tac Asp Ala Lys Ser Cys Ala Gln Asn Cys Cys Val Asp Gly Ala Asp Tyr 85 90 95	288
acc agc acc tat ggc atc acc acc aac ggt gat tcc ctg agc ctc aag Thr Ser Thr Tyr Gly Ile Thr Thr Asn Gly Asp Ser Leu Ser Leu Lys 100 105 110	336
ttc gtc acc aag ggc cag cac tcg acc aac gtc ggc tcg cgt acc tac Phe Val Thr Lys Gly Gln His Ser Thr Asn Val Gly Ser Arg Thr Tyr 115 120 125	384
ctg atg gac ggc gag gac aag tat cag acc ttc gag ctc ctc ggc aac Leu Met Asp Gly Glu Asp Lys Tyr Gln Thr Phe Glu Leu Leu Gly Asn 130 135 140	432
gag ttc acc ttc gat gtc gat gtc tcc aac atc ggc tgc ggt ctc aac Glu Phe Thr Phe Asp Val Asp Val Ser Asn Ile Gly Cys Gly Leu Asn 145 150 155 160	480
ggc gcc ctg tac ttc gtc tcc atg gac gcc gat ggt ggt ctc agc cgc Gly Ala Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Leu Ser Arg 165 170 175	528
tat cct ggc aac aag gct ggt gcc aag tac ggt acc ggc tac tgc gat Tyr Pro Gly Asn Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp 180 185 190	576
gct cag tgc ccc cgt gac atc aag ttc atc aac ggc gag gcc aac att Ala Gln Cys Pro Arg Asp Ile Lys Phe Ile Asn Gly Glu Ala Asn Ile 195 200 205	624
gag ggc tgg acc ggc tcc acc aac gac ccc aac gcc ggc gcg ggc cgc Glu Gly Trp Thr Gly Ser Thr Asn Asp Pro Asn Ala Gly Ala Gly Arg 210 215 220	672
tat ggt acc tgc tgc tct gag atg gat atc tgg gaa gcc aac aac atg Tyr Gly Thr Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Asn Met 225 230 235 240	720
gct act gcc ttc act cct cac cct tgc acc atc att ggc cag agc cgc Ala Thr Ala Phe Thr Pro His Pro Cys Thr Ile Ile Gly Gln Ser Arg	768

245				250				255								
tgc	gag	ggc	gac	tcg	tgc	ggc	ggc	acc	tac	agc	aac	gag	cgc	tac	gcc	816
Cys	Glu	Gly	Asp	Ser	Cys	Gly	Gly	Thr	Tyr	Ser	Asn	Glu	Arg	Tyr	Ala	
260				265				270								
ggc	gtc	tgc	gac	ccc	gat	ggc	tgc	gac	ttc	aac	tcg	tac	cgc	cag	ggc	864
Gly	Val	Cys	Asp	Pro	Asp	Gly	Cys	Asp	Phe	Asn	Ser	Tyr	Arg	Gln	Gly	
275				280				285								
aat	aag	acc	ttc	tac	ggc	aag	ggc	atg	acc	gtc	gac	acc	acc	aag	aag	912
Asn	Lys	Thr	Phe	Tyr	Gly	Lys	Gly	Met	Thr	Val	Asp	Thr	Thr	Lys	Lys	
290				295				300								
atc	act	gtc	gtc	acc	cag	ttc	ctc	aag	gat	gcc	aac	ggc	gat	ctc	ggc	960
Ile	Thr	Val	Val	Thr	Gln	Phe	Leu	Lys	Asp	Ala	Asn	Gly	Asp	Leu	Gly	
305				310				315				320				
gag	gtc	aag	cgc	ttc	tac	gtc	cag	gat	ggc	aag	atc	atc	ccc	aac	tcc	1008
Glu	Val	Lys	Arg	Phe	Tyr	Val	Gln	Asp	Gly	Lys	Ile	Ile	Pro	Asn	Ser	
325				330				335								
gag	tcc	acc	atc	ccc	ggc	gtc	gag	ggc	aat	tcc	atc	acc	cag	gac	tgg	1056
Glu	Ser	Thr	Ile	Pro	Gly	Val	Glu	Gly	Asn	Ser	Ile	Thr	Gln	Asp	Trp	
340				345				350								
tgc	gac	cgc	cag	aag	gtt	gcc	ttt	ggc	gac	att	gac	gac	ttc	aac	cgc	1104
Cys	Asp	Arg	Gln	Lys	Val	Ala	Phe	Gly	Asp	Ile	Asp	Asp	Phe	Asn	Arg	
355				360				365								
aag	ggc	ggc	atg	aag	cag	atg	ggc	aag	gcc	ctc	gcc	ggc	ccc	atg	gtc	1152
Lys	Gly	Gly	Met	Lys	Gln	Met	Gly	Lys	Ala	Leu	Ala	Gly	Pro	Met	Val	
370				375				380								
ctg	gtc	atg	tcc	atc	tgg	gat	gac	cac	gcc	tcc	aac	atg	ctc	tgg	ctc	1200
Leu	Val	Met	Ser	Ile	Trp	Asp	Asp	His	Ala	Ser	Asn	Met	Leu	Trp	Leu	
385				390				395				400				
gac	tcg	acc	ttc	cct	gtc	gat	gcc	gct	ggc	aag	ccc	ggc	gcc	gag	cgc	1248
Asp	Ser	Thr	Phe	Pro	Val	Asp	Ala	Ala	Gly	Lys	Pro	Gly	Ala	Glu	Arg	
405				410				415								
ggc	gcc	tgc	ccg	acc	acc	tcg	ggc	gtc	cct	gct	gag	gtt	gag	gcc	gag	1296
Gly	Ala	Cys	Pro	Thr	Thr	Ser	Gly	Val	Pro	Ala	Glu	Val	Glu	Ala	Glu	
420				425				430								
gcc	ccc	aac	agc	aac	gtc	gtc	ttc	tcc	aac	atc	cgc	ttc	ggc	ccc	atc	1344
Ala	Pro	Asn	Ser	Asn	Val	Val	Phe	Ser	Asn	Ile	Arg	Phe	Gly	Pro	Ile	
435				440				445								
ggc	tcg	acc	gtt	gct	ggc	ctc	ccc	ggc	gag	ggc	aac	ggc	ggc	aac	aac	1392
Gly	Ser	Thr	Val	Ala	Gly	Leu	Pro	Gly	Ala	Gly	Asn	Gly	Gly	Asn	Asn	
450				455				460								
ggc	ggc	aac	ccc	ccg	ccc	ccc	acc	acc	acc	acc	tcc	tcg	gct	ccg	gcc	1440
Gly	Gly	Asn	Pro	Pro	Pro	Pro	Thr	Thr	Thr	Thr	Ser	Ser	Ala	Pro	Ala	
465				470				475				480				
acc	acc	acc	acc	gcc	agc	gct	ggc	ccc	aag	gct	ggc	cac	tgg	cag	cag	1488
Thr	Thr	Thr	Thr	Ala	Ser	Ala	Gly	Pro	Lys	Ala	Gly	His	Trp	Gln	Gln	
485				490				495								

tgc ggc ggc atc ggc ttc act ggc ccg acc cag tgc gag gag ccc tac 1536
 Cys Gly Gly Ile Gly Phe Thr Gly Pro Thr Gln Cys Glu Glu Pro Tyr
 500 505 510

act tgc acc aag ctc aac gac tgg tac tct cag tgc ctg taa 1578
 Thr Cys Thr Lys Leu Asn Asp Trp Tyr Ser Gln Cys Leu
 515 520 525

<210> 60
 <211> 525
 <212> PRT
 <213> Scytalidium thermophilum

<400> 60

Met Arg Thr Ala Lys Phe Ala Thr Leu Ala Ala Leu Val Ala Ser Ala
 1 5 10 15

Ala Ala Gln Gln Ala Cys Ser Leu Thr Thr Glu Arg His Pro Ser Leu
 20 25 30

Ser Trp Lys Lys Cys Thr Ala Gly Gly Gln Cys Gln Thr Val Gln Ala
 35 40 45

Ser Ile Thr Leu Asp Ser Asn Trp Arg Trp Thr His Gln Val Ser Gly
 50 55 60

Ser Thr Asn Cys Tyr Thr Gly Asn Lys Trp Asp Thr Ser Ile Cys Thr
 65 70 75 80

Asp Ala Lys Ser Cys Ala Gln Asn Cys Cys Val Asp Gly Ala Asp Tyr
 85 90 95

Thr Ser Thr Tyr Gly Ile Thr Thr Asn Gly Asp Ser Leu Ser Leu Lys
 100 105 110

Phe Val Thr Lys Gly Gln His Ser Thr Asn Val Gly Ser Arg Thr Tyr
 115 120 125

Leu Met Asp Gly Glu Asp Lys Tyr Gln Thr Phe Glu Leu Leu Gly Asn
 130 135 140

Glu Phe Thr Phe Asp Val Asp Val Ser Asn Ile Gly Cys Gly Leu Asn
 145 150 155 160

Gly Ala Leu Tyr Phe Val Ser Met Asp Ala Asp Gly Gly Leu Ser Arg
 165 170 175

Tyr Pro Gly Asn Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp
 180 185 190

Ala Gln Cys Pro Arg Asp Ile Lys Phe Ile Asn Gly Glu Ala Asn Ile
 195 200 205

Glu Gly Trp Thr Gly Ser Thr Asn Asp Pro Asn Ala Gly Ala Gly Arg
 210 215 220

Tyr Gly Thr Cys Cys Ser Glu Met Asp Ile Trp Glu Ala Asn Asn Met
 225 230 235 240

Ala Thr Ala Phe Thr Pro His Pro Cys Thr Ile Ile Gly Gln Ser Arg

	245		250		255										
Cys	Glu	Gly	Asp	Ser	Cys	Gly	Gly	Thr	Tyr	Ser	Asn	Glu	Arg	Tyr	Ala
	260							265					270		
Gly	Val	Cys	Asp	Pro	Asp	Gly	Cys	Asp	Phe	Asn	Ser	Tyr	Arg	Gln	Gly
		275					280					285			
Asn	Lys	Thr	Phe	Tyr	Gly	Lys	Gly	Met	Thr	Val	Asp	Thr	Thr	Lys	Lys
	290					295					300				
Ile	Thr	Val	Val	Thr	Gln	Phe	Leu	Lys	Asp	Ala	Asn	Gly	Asp	Leu	Gly
305					310					315					320
Glu	Val	Lys	Arg	Phe	Tyr	Val	Gln	Asp	Gly	Lys	Ile	Ile	Pro	Asn	Ser
				325					330					335	
Glu	Ser	Thr	Ile	Pro	Gly	Val	Glu	Gly	Asn	Ser	Ile	Thr	Gln	Asp	Trp
			340					345					350		
Cys	Asp	Arg	Gln	Lys	Val	Ala	Phe	Gly	Asp	Ile	Asp	Asp	Phe	Asn	Arg
		355					360					365			
Lys	Gly	Gly	Met	Lys	Gln	Met	Gly	Lys	Ala	Leu	Ala	Gly	Pro	Met	Val
	370					375					380				
Leu	Val	Met	Ser	Ile	Trp	Asp	Asp	His	Ala	Ser	Asn	Met	Leu	Trp	Leu
385					390					395					400
Asp	Ser	Thr	Phe	Pro	Val	Asp	Ala	Ala	Gly	Lys	Pro	Gly	Ala	Glu	Arg
				405					410					415	
Gly	Ala	Cys	Pro	Thr	Thr	Ser	Gly	Val	Pro	Ala	Glu	Val	Glu	Ala	Glu
			420					425					430		
Ala	Pro	Asn	Ser	Asn	Val	Val	Phe	Ser	Asn	Ile	Arg	Phe	Gly	Pro	Ile
		435					440					445			
Gly	Ser	Thr	Val	Ala	Gly	Leu	Pro	Gly	Ala	Gly	Asn	Gly	Gly	Asn	Asn
	450					455					460				
Gly	Gly	Asn	Pro	Pro	Pro	Pro	Thr	Thr	Thr	Thr	Ser	Ser	Ala	Pro	Ala
465					470				475						480
Thr	Thr	Thr	Thr	Ala	Ser	Ala	Gly	Pro	Lys	Ala	Gly	His	Trp	Gln	Gln
				485					490					495	
Cys	Gly	Gly	Ile	Gly	Phe	Thr	Gly	Pro	Thr	Gln	Cys	Glu	Glu	Pro	Tyr
			500					505					510		
Thr	Cys	Thr	Lys	Leu	Asn	Asp	Trp	Tyr	Ser	Gln	Cys	Leu			
	515						520					525			

<210> 61
 <211> 519
 <212> DNA
 <213> Aspergillus sp.

<220>
 <221> misc_feature

<222> (1)..(519)

<223> Partial CBH1 encoding sequence

<400> 61

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gagatggaca tatgggagggc caacagcatc tccacggcct tcacgccccca cccctgcgat      60
gtccccggcc aggtgatgtg cgagggcgac tcctgcggtg gcacctacag cagcgaccgc      120
tatggcggca cctgcgatcc cgatggatgt gacttcaact cctaccgcca gggcaacaag      180
tccttctacg gccccggcat gaccgtcgac accaacagca aggtcaccgt cgtgactcag      240
ttcctcaccg acgacggcac tgccaccggc accctgtcgg agatcaagcg gttctacgtg      300
cagaacggca aggtcatccc caactccgag tcgacctggc ccggcgtcgg cggcaactcc      360
atcaccaccg actactgtct ggcccagaag agcctcttcg gcgataccga cgtcttcacc      420
aagcacggcg gtatggaggg catgggcgcc gccctcgccg agggcatggg cctcgtcctg      480
agtctctggg acgaccacca ctccaacatg ctctggctg      519

```

<210> 62

<211> 497

<212> DNA

<213> Scopulariopsis sp.

<220>

<221> misc_feature

<222> (1)..(497)

<223> Partial CBH1 encoding sequence

<400> 62

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gagatcgatg tgtgggagtc gaacgcctat gccttcgttt tcacgccgca cgcgtgcacg      60
accaacgagt accacgtctg cgagaccacc aactgcggtg gcacctactc ggaggaccgc      120
ttcaccggca agtgcgacgc caacggctgc gactacaacc cctaccgcat gggcaacccc      180
gacttctacg gcaagggcaa gacgctcgac accagccgca agttcaccgt cgtctcccgc      240
ttcgaggaga acaagctctc ccagtacttc atccaggacg gccgcaagat cgagatcccg      300
ccgccgacgt gggaggggcat gcccaacagc agcgagatca cccccgagct ctgctccacc      360
atgttcgatg tgctcgacga ccgcaaccgc ttgcaggagg tcggcggctt cgagcagctg      420
aacaacgccc tccgggttcc catgggtcctc gtcatgtcca tctgggacga ccactacgcc      480
aacatgctct ggctcga      497

```

<210> 63

<211> 498

<212> DNA

<213> Fusarium sp.

<220>

<221> misc_feature

<222> (1)..(498)

<223> Partial CBH1 encoding sequence

<400> 63

```

gagatggata tctgggaggc caacaagatc tccactgcct acactcccca cccctgcaag      60
agcctcaccc agcagtcctg cgagggcgat gcctgcggtg gcacctactc tactaccgcg      120
tatgctggaa cttgcgaccc cgatgggttg gatttcaacc cttaccgcca gggcaacaag      180
accttctacg gccccggctc cggcttcaac gttgatacca ccaagaaggt gactgtcgtg      240
accagttca tcaagggcag cgacggcaag ctttccgaga tcaagcgtct ctatgttcag      300
aatggcaagg tcattggcaa cccccagtct gagattgcca gcaaccctgg cagcagcgtc      360
accgacagct tctgcaaggc ccagaagggt gccttcaacg accccgatga cttcaacaag      420
aaggggtggct ggagcggaat gagcgacgcc ctgcgaagc ccatgggttct cgtcatgagc      480
ttgtggcacg acgtgagt                                     498

```

<210> 64

<211> 525

<212> DNA

<213> Verticillium sp.

<220>

<221> misc_feature

<222> (1)..(525)

<223> Partial CBH1 encoding sequence

<400> 64

```

gagatggata tctgggaggc caacaagatc tccacggcct acactcccca tccctgcaag      60
agcctcaccc agcagtcctg tgagggcgat gcctgcggtg gcacctactc ttccaccgcg      120
tatgctggaa cttgcgatcc cgatgggtgc gatttcaacc cttaccgcca gggcaaccac      180
accttctacg gtcccggctc cggcttcaac gtcgatacca ccaagaaggt gactgtcgtg      240
accagttca tcaagggcag cgacggcaag ctttccgaga tcaagcgtct ctatgttcag      300
aatggcaagg tcacggcaa cccccagtcc gagattgcaa acaaccccg gagctccgtc      360
accgacagct tctgcaaggc ccagaagggt gccttcaacg accccgatga cttcaacaag      420
aaggggtggct ggagcggcat gaacgacgcc ctgcgaagc ccatgggttct cgtcatgagc      480
ctgtggcacg acgtgagtaa tctaaccctt gagtctcgga caaga                                     525

```

<210> 65

<211> 1371

<212> DNA

<213> Pseudoplectania nigrella

<220>

<221> CDS

<222> (1) .. (1371)

<223>

<400> 65

atg cta tcc aat ctc ctt ctc tca ctc tct ttc ctt tcc cta gcc tcc	48
Met Leu Ser Asn Leu Leu Leu Ser Leu Ser Phe Leu Ser Leu Ala Ser	
1 5 10 15	
ggg caa aac atc ggt acc aac acc gcc gaa agc cac ccc caa ctt cgt	96
Gly Gln Asn Ile Gly Thr Asn Thr Ala Glu Ser His Pro Gln Leu Arg	
20 25 30	
tct caa acc tgc acc aaa ggc aac gga tgc agc acc caa tcc acc tcc	144
Ser Gln Thr Cys Thr Lys Gly Asn Gly Cys Ser Thr Gln Ser Thr Ser	
35 40 45	
gta gtc ctg gac tcc aac tgg cgc tgg ctg cac aat aat gga ggt tca	192
Val Val Leu Asp Ser Asn Trp Arg Trp Leu His Asn Asn Gly Gly Ser	
50 55 60	
acg aac tgc tac acc ggc aat tcc tgg gac tct aca tta tgt ccc gac	240
Thr Asn Cys Tyr Thr Gly Asn Ser Trp Asp Ser Thr Leu Cys Pro Asp	
65 70 75 80	
cca gtt acc tgc gcc aag aac tgt gct ctc gac ggt gcc gac tat tct	288
Pro Val Thr Cys Ala Lys Asn Cys Ala Leu Asp Gly Ala Asp Tyr Ser	
85 90 95	
ggg aca tac gga atc acc tct acg gga gat gct ttg acg ttg aag ttt	336
Gly Thr Tyr Gly Ile Thr Ser Thr Gly Asp Ala Leu Thr Leu Lys Phe	
100 105 110	
gtt act cag ggt cct tat tcg act aat att gga tct cgg gta tac cta	384
Val Thr Gln Gly Pro Tyr Ser Thr Asn Ile Gly Ser Arg Val Tyr Leu	
115 120 125	
atg gcg agt gat act cag tat aag atg ttc cag ctc aag aac aag gag	432
Met Ala Ser Asp Thr Gln Tyr Lys Met Phe Gln Leu Lys Asn Lys Glu	
130 135 140	
ttt acg ttt gat gtt gat gtc tct aat ctt cct tgt gga tta aac gga	480
Phe Thr Phe Asp Val Asp Val Ser Asn Leu Pro Cys Gly Leu Asn Gly	
145 150 155 160	
gcg ttg tat ttt gtg gag atg gat gcg gat gga gga atg tcg aaa tac	528
Ala Leu Tyr Phe Val Glu Met Asp Ala Asp Gly Gly Met Ser Lys Tyr	
165 170 175	
ccg tct aat aaa gcc ggg gca aaa tat gga acc ggg tat tgt gat gcg	576
Pro Ser Asn Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ala	
180 185 190	
cag tgt cca cat gat atc aaa ttt atc aac ggg gag gca aat ctc cta	624
Gln Cys Pro His Asp Ile Lys Phe Ile Asn Gly Glu Ala Asn Leu Leu	
195 200 205	
gac tgg acg cct tca acc agc gac aaa aat gcc ggc tcc gga cgt tac	672
Asp Trp Thr Pro Ser Thr Ser Asp Lys Asn Ala Gly Ser Gly Arg Tyr	
210 215 220	
ggg acc tgt tgt caa gaa atg gac atc tgg gaa gcc aac agc atg gca	720

Gly 225	Thr	Cys	Cys	Gln	Glu 230	Met	Asp	Ile	Trp	Glu 235	Ala	Asn	Ser	Met	Ala 240	
acc	gcc	tat	aca	ccg	cat	ccc	tgt	agt	gtc	tca	gga	cct	acc	cga	tgc	768
Thr	Ala	Tyr	Thr	Pro	His	Pro	Cys	Ser	Val	Ser	Gly	Pro	Thr	Arg	Cys	
				245					250					255		
tca	gga	acc	caa	tgt	ggg	gat	ggg	tct	aac	cgt	cat	aac	gga	att	tgc	816
Ser	Gly	Thr	Gln	Cys	Gly	Asp	Gly	Ser	Asn	Arg	His	Asn	Gly	Ile	Cys	
			260					265					270			
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Asp	Lys	Asp	Gly	Cys	Asp	Phe	Asn	Ser	Tyr	Arg	Met	Gly	Asn	Thr	Thr	
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Phe	Phe	Gly	Lys	Gly	Ala	Thr	Val	Asn	Thr	Asn	Ser	Lys	Phe	Thr	Val	
	290					295					300					
gta	acg	caa	ttc	atc	acc	tcc	gac	aac	acc	tca	act	gga	gcg	cta	aag	960
Val	Thr	Gln	Phe	Ile	Thr	Ser	Asp	Asn	Thr	Ser	Thr	Gly	Ala	Leu	Lys	
305					310					315					320	
gag	att	cgt	cgt	ctt	tat	att	cag	aat	gga	aaa	gtc	atc	cag	aac	tcg	1008
Glu	Ile	Arg	Arg	Leu	Tyr	Ile	Gln	Asn	Gly	Lys	Val	Ile	Gln	Asn	Ser	
				325					330					335		
aaa	agt	aat	atc	tcc	ggc	atg	tca	gct	tac	gac	tct	ata	acc	gag	gat	1056
Lys	Ser	Asn	Ile	Ser	Gly	Met	Ser	Ala	Tyr	Asp	Ser	Ile	Thr	Glu	Asp	
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Phe	Cys	Ala	Ala	Gln	Lys	Thr	Ala	Phe	Gly	Asp	Thr	Asn	Asp	Phe	Lys	
		355					360					365				
gca	aag	ggc	gga	ttt	aca	aac	ctt	ggg	aat	gcg	ttg	caa	aag	gga	atg	1152
Ala	Lys	Gly	Gly	Phe	Thr	Asn	Leu	Gly	Asn	Ala	Leu	Gln	Lys	Gly	Met	
	370					375					380					
gtt	ttg	gcg	ttg	agt	att	tgg	gat	gat	cat	gct	gcg	cag	atg	ctt	tgg	1200
Val	Leu	Ala	Leu	Ser	Ile	Trp	Asp	Asp	His	Ala	Ala	Gln	Met	Leu	Trp	
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Leu	Asp	Ser	Ser	Tyr	Pro	Leu	Asp	Lys	Asp	Pro	Ser	Gln	Pro	Gly	Val	
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aag	agg	ggc	gcg	tgt	gct	acc	tct	tct	ggg	aaa	ccg	tcg	gat	gtc	gag	1296
Lys	Arg	Gly	Ala	Cys	Ala	Thr	Ser	Ser	Gly	Lys	Pro	Ser	Asp	Val	Glu	
			420					425					430			
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Asn	Gln	Ser	Pro	Asn	Ala	Ser	Val	Thr	Phe	Ser	Asn	Ile	Lys	Phe	Gly	
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gat	att	gga	tcg	act	tat	tcc	tct	tag								1371
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<211> 456

<212> PRT

<213> Pseudoplectania nigrella

<400> 66

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Ser Gln Thr Cys Thr Lys Gly Asn Gly Cys Ser Thr Gln Ser Thr Ser
35          40          45

Val Val Leu Asp Ser Asn Trp Arg Trp Leu His Asn Asn Gly Gly Ser
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Thr Asn Cys Tyr Thr Gly Asn Ser Trp Asp Ser Thr Leu Cys Pro Asp
65          70          75          80

Pro Val Thr Cys Ala Lys Asn Cys Ala Leu Asp Gly Ala Asp Tyr Ser
85          90          95

Gly Thr Tyr Gly Ile Thr Ser Thr Gly Asp Ala Leu Thr Leu Lys Phe
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Val Thr Gln Gly Pro Tyr Ser Thr Asn Ile Gly Ser Arg Val Tyr Leu
115         120         125

Met Ala Ser Asp Thr Gln Tyr Lys Met Phe Gln Leu Lys Asn Lys Glu
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Phe Thr Phe Asp Val Asp Val Ser Asn Leu Pro Cys Gly Leu Asn Gly
145         150         155         160

Ala Leu Tyr Phe Val Glu Met Asp Ala Asp Gly Gly Met Ser Lys Tyr
165         170         175

Pro Ser Asn Lys Ala Gly Ala Lys Tyr Gly Thr Gly Tyr Cys Asp Ala
180         185         190

Gln Cys Pro His Asp Ile Lys Phe Ile Asn Gly Glu Ala Asn Leu Leu
195         200         205

Asp Trp Thr Pro Ser Thr Ser Asp Lys Asn Ala Gly Ser Gly Arg Tyr
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Gly Thr Cys Cys Gln Glu Met Asp Ile Trp Glu Ala Asn Ser Met Ala
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Thr Ala Tyr Thr Pro His Pro Cys Ser Val Ser Gly Pro Thr Arg Cys
245         250         255

Ser Gly Thr Gln Cys Gly Asp Gly Ser Asn Arg His Asn Gly Ile Cys
260         265         270

Asp Lys Asp Gly Cys Asp Phe Asn Ser Tyr Arg Met Gly Asn Thr Thr
275         280         285

Phe Phe Gly Lys Gly Ala Thr Val Asn Thr Asn Ser Lys Phe Thr Val
290         295         300

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Val Thr Gln Phe Ile Thr Ser Asp Asn Thr Ser Thr Gly Ala Leu Lys
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 Glu Ile Arg Arg Leu Tyr Ile Gln Asn Gly Lys Val Ile Gln Asn Ser
 325 330 335
 Lys Ser Asn Ile Ser Gly Met Ser Ala Tyr Asp Ser Ile Thr Glu Asp
 340 345 350
 Phe Cys Ala Ala Gln Lys Thr Ala Phe Gly Asp Thr Asn Asp Phe Lys
 355 360 365
 Ala Lys Gly Gly Phe Thr Asn Leu Gly Asn Ala Leu Gln Lys Gly Met
 370 375 380
 Val Leu Ala Leu Ser Ile Trp Asp Asp His Ala Ala Gln Met Leu Trp
 385 390 395 400
 Leu Asp Ser Ser Tyr Pro Leu Asp Lys Asp Pro Ser Gln Pro Gly Val
 405 410 415
 Lys Arg Gly Ala Cys Ala Thr Ser Ser Gly Lys Pro Ser Asp Val Glu
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 <213> *Phytophthora infestans*

<220>
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 <223> Partial CBH1 encoding sequence

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